PTO-1590 (1-2000)

SEARCH (REQUEST FORM Control and Second Callinformation Center

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Requester's Full Name: <u>KAREN</u> Art Unit: 1642 Phone N	mber 30.6 771.7	Examiner # :_//6.8/ Serial Number: 69	Date: 8/28	<u>/0/</u>
Mail Box and Bldg/Room Location:	87 63 Resul	ts Format Preferred (circle)	PAPER) DISK	E-MAIL
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If more than one search is submi	tted, please prioritize	searches in order of in	eed. ************	****
Please provide a detailed statement of the s	earch topic, and describe as	specifically as possible the sul	ject matter to be sea	rched.
Include the elected species or structures, ke utility of the invention. Define any terms to				
known. Please attach a copy of the cover sh			nt citations, authors,	eic, 11
Title of Invention:			CN.	43
Inventors (please provide full names):			χ_{\sim}	
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Fron Sequence Searches Only Please include	all pertinent information (po	rent, child, divisional, or issued p	oatent numbers) along	with the
appropriate serial number.				
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Searcher Location: 13/10/10/10/10	Structure (#)	Questel/Orbit		<u></u>
Date Searcher Picked Up: 8/28/07	Bibliographic	Dr Link		<u> </u>
Date Completed: 8/3////	Litigation	Lexis/Nexis		<u> </u>
Searcher Prep & Review Time:	Fulltext	Sequence Systems	52	
Clerical Prep Time: 5	Patent Family	WWW/Internet		
Online Time: 3	Other	Other (specify)	<u> </u>	<u> </u>

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Result
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	8	Sequence 8, Appli	714	e 14,	Sequence 14, Appl	598,	2597,	2596,	857,	934,	250,		214, A	2595,	2599,	479,	777,	776,	~	4178	e 12,	Sequence 12, Appl	Sequence 15807, A	N	1573		e 16346	e 700, A	198	e 1,	e 2,	e 5,	,2	e 4,	2

ALIGNMENTS

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APPLICANT: LUBORAT, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Lesage, Florian
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASS (134] CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY RETHER CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY RETHER OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-01-15
EARLIER FILING DATE: 1996-01-15
EARLIER FILING DATE: 1996-01-04
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 394
TYDE: DRT
; FEATURE:
; OTHER INFORMATION: TASK
US-09-144-914-4
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US-09-144-914-4
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                                                                  LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
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Query Match Best Local Similarity Matches 394; Conserv

Conservative

100.0%; Score 2042; i. 100.0%; Pred. No. 1.^. tive 0; Mismatches

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Indels Length 394;

0,

Gaps

300

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APPLICANT: FARMAN, NICOLETTE
APPLICANT: LAZDUNSKI, MICHEL
TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THE
TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCRE
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-01-09
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE
TOTHER INFORMATION: TASK
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GENERAL INFORMATION:
APPLICANT: REYES, ROBERTO
APPLICANT: DUPRAT, FABRICE
                                                                                                         Query Match 100.0%; Score 2042; DB 18; Best Local Similarity 100.0%; Pred. No. 1.9e-197; Matches 394; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORTIAN
APPLICANT: LESAGE, FLORTIAN
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identific; or FILE REFERENCE: f17b2prov3-humanTREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT ETLING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 5
LENGTH: 394
TYPE: PRT
ORGANISM: Mus sp.
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CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

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APPLICANT: HONORE, ERIC
APPLICANT: HONORE, ERIC
APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: DIPRAT, FABRICE
TITLE OF INVENTION: MCCHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
FILE REFERENCE: 1383-00
CURRENT APPLICATION NUMBER: US/09/655,272
CURRENT APPLICATION NUMBER: PCT/FR99/00404
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR FILING DATE: 1998-02-23
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 394
TYDE: DRT
RESULT 5
US-09-144-914-5
; Sequence 5, Application US/09144914;
; GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Unknown
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APPLICANT: LIZIONSKI, MICHEL
APPLICANT: LAZDONSKI, MICHEL
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHA
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY OR THE
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER APPLICATION NUMBER: PR 96/015
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US-09-436-265-5
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Sequence 5, Application US/09436265

GENERAL INFORMATION:
APPLICANT: REYES, ROBERTO
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: SALINAS, MIGUEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: LAZDUNSKI, MICHEL
TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN PARTICLS, THEIR
TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIFALLY FOR THE SCREENING
TITLE OF INVENTION: DRUGS
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Best Local (
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APPLICANT: Lesage, Flor
APPLICANT: Fink, Michel
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ORGANISM: Murine
FEATURE:
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357; Conserv
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Florian
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88.1%;
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Pred. No. 7.6e
9; Mismatches
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PRIOR APPLICATION NUMBER: 60/095,234
PRIOR ETLING DATE: 1998-08-04
PRIOR PELING DATE: 1998-08-04
PRIOR APPLICATION UNMBER: 60/107,692
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 405
TYPE: PRT
ORGANISM: Murine sp.
FEATURE:
OTHER INFORMATION: TASK
US-09-436-265-5
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                                                                                                                                                                                                                                                             Sequence 55, Application US/08816011C
GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
                                 SEQ ID NO 55
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity 88.1%;
                                                                                                                                                                                 APPLICANT: Price, Laura A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLECTIDE SEQUENCES ENCODING
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-11
                                                                                        PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
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CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
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Pred. No. 7.6e-175;
9; Mismatches 25;
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US-08-816-011C-62
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Best Local Similarity
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SOFTWARE: PatentIn Ver.
SEQ ID NO 62
LENGTH: 309
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APPLICANT: Price, Laura A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 VYLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGG-------GGSAHTTDTASSTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVA<sup>†</sup> FVYILTGLTVIG--AFLNL 241
                                                   184 WTFEQAYYYCFITLTTIGEGDYVALQKDQALQTQPQYVAES YYILTGLTVIG--AFLNL 241
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                           WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVASA; SCTSSRAHGHRRFLNL 249
                                                                                                                                                                                                                            ENVRTLALIVCTFTYLLVGAAVFDALESEPEMIERORU
                                                                                                      MFQSLGERINTSVRYLLHRAKRGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSYYER 192
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83.9%;
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Pred. No. 6.7
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... GSAHTTDTASSTAAA 291
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US-08-816-011-55
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, '
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: Parsippany
CITY: Parsippany
CTATE: New Jersey
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CORRESPONDENCE ADDRESS:
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310 A 310
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                                                                                                                                                       181 YEHWTEFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIG--AF 238
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STRANDEDNESS: sin
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                  13 ENVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLELRARYNLSEGGYEELE 72
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                                   A 291
                                                                    LNLVVLRFMTMNAEDEKRDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAA
                                                                                                     LNLVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGG------GGSAHTTDTASSTAA 290
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                                                                                                                                       YERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVASA---SCTSSRAHGHRRF
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Encoding Them, and Methods of Using Same
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83.1%;
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Pred. No. 9.9e-115;
8; Mismatches 27;
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US-08-816-011A-55
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Best Local Similarity 83.1%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Parsippany
CTATE: New Jersey
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NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,
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CORRESPONDENCE ADDRESS:
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                                                                                     291 A 291
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                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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TELEFAX: 201-683-4117
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                                                           A 310
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Sequence 2, Application US/09516279

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Sequence 4, Application US/09516279
GENERAL INFORMATION:
APPLICANT: David M. Duckworth
APPLICANT: Robert J. Godden
APPLICANT: Conrad G. Chapman
APPLICANT: Helen J. Meadows
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30200
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Best Local Similarity
Matches 233; Conserv
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APPLICANT: David M. Duckworth
             CURRENT APPLICATION NUMBER: US/09/516,279
CURRENT FILING DATE: 2000-03-01
EARLIER APPLICATION NUMBER: UK 9905061.9
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: UK 0003112.0
EARLIER FILING DATE: 2000-02-09
MUMBER OF SED ID NOS: 4
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CURRENT FILING DATE: 2000-03-01
EARLIER APPLICATION NUMBER: UK 9905061.9
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: UK 0003112.0
EARLIER FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30200
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ORGANISM: HOMO SAPIENS
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Query Match Best Local S Matches 233

Local Similarity les 233; Conserv

54.7%; 59.0%;

Score 1116; DB 13: Pred. No. 1.1e-

Length 374;

Gaps

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MKRQNVRTLSLIVCTFTYLLVGAAVFDALESDHEMREEEKLKAEEIRIKGKYNISSEDYR

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472584CD1
US-60-199-020-2
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-516-279-4
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LENGTH: 374
TYPE: PRT
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TENGTH: 374
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APPLICANT: Nguyen, Danniel B.
APPLICANT: Policky, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION
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                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/199,020
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                 FILE REFERENCE: PI-0073 P
                                                                  ORGANISM: Homo sapiens
                                                    FEATURE:
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                                                                                                                                 PERL Program
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Yao, Monique G.
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Baughn, Mariah R.
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59.0%;
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Pred. No. 1.1e-103;
4; Mismatches 9;
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-518-866-5
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GENERAL INFORMATION:
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Best Local
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APPLICANT: Glucksmann, Maria A
TITLE OF INVENTION: A NOVEL POTASSIUM CHANNEL MOLECULE AND USES THEREFOR
FILE REFERENCE: MNI-093
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Search completed: August 28, 2001, Job time: 604 sec

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Sequence 2, Application US/09518866 GENERAL INFORMATION:

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 400 .
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Best Local Similarity
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CURRENT FILING DATE: 2000-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CUTTIS, ROTY J
APPLICANT: GUTTIS, ROTY J
TITLE OF INVENTION: A NOVEL POTASSIUM CHANNEL PRICULE AND USES
FILE REFERENCE: MNI-093
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                                                                 181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPOYV
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                              241 LVVLRFMTMNAEDEKRDA 258
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                                                               FEGWTFFHAYYYCFITLTTIGFGDFVALQSGEALQRKLP\\.:\SFLYILLGLTVIGAFLN 310
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LVVLRFLVASADWPERAA
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1: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen
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US-09-331-3678-1
US-09-431-3678-1
US-09-431-3678-1
US-09-336-643-10
US-09-336-643-10
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Sequence 15, Appli Sequence 61, Appli Sequence 60, Appli Sequence 58, Appli Sequence 58, Appli Sequence 22, Appli Sequence 83, Appli Sequence 81, Appli Sequence 81, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1386, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 10, 
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APPLICANT: Powers, Scott
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A NOVel Potassium
FILE REFERENCE: 0.18781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 394
TYPE: PRT
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FEATURE:
OTHER INFORMATION: human potassium
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Best Local Similarity
Matches 394; Conserv
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Result

Minimum Maximum

Database

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Sequence 61, Application US/09746491

GENERAL INFORMATION:

APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: Novel Proteins and Nucleic Aci
FILE REFERENCE: 15966-621

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: USSN 60/171,329

PRIOR APPLICATION NUMBER: USSN 60/171,329

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 61

LENGTH: 258

TYPE: DET
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US-09-798-584-1
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                                                                   SEQ ID NO 1
LENGTH: 374
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Best Local Similarity
                                                                                                                                                           APPLICANT: Mu, David
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584.
CURRENT FILING DATE: 2001-03-03
                                                                                                                   PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
                                                                                                    SOFTWARE: PatentIn Ver. 2.1
FEATURE:
OTHER INFORMATION: human KCNB (Potassium Channel
                                  ORGANISM: Homo sapiens
                                                        TYPE: PRT
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; ORGANISM: Cavia porcellus
US-09-746-491-60
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 60
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Matches 233; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILLING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 15966-621
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tes 226; Conserv
                                                                                                                                                              YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVA. SEVYILTGLTVIGAFLN
                                  TLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTEVSMENMV! / 3FFSCMGTLC1GAAAFSQ 180
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59.08;
                                                                                                                                                                                                                             52.4%; Score 1069.5; 57.1%; Pred. No. 6e-8%; tive 43; Mismatches
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181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQY
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US-09-746-491-59

Sequence 59, Application US/09746491

GENERAL INFORMATION:

APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-621

CURRENT APPLICATION NUMBER: US/09/746,491

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: USN 60/171,329

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 72

SECTION OF SECTION SECTION SECTION SECTION NUMBER: US SOFTWARE: Patentin Ver. 2.0
                                                                                                                            US-09-746-491-58; Sequence 58, Application US/09746491; GENERAL INFORMATION:
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Best Local Similarity
Matches 167; Conserv
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LENGTH: 330
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-09-746-491-59
             CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
                                                                             APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Novel Proteins and Nucleic FILE REFERENCE: 15966-621
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                                                                                                                                                                                                                                  LVVLRFLVASADWPERAA
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ID NOS:
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SEQ ID NO 58
LENGTH: 330
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Matches
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Best Local Similarity
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: VARIANT
LOCATION: (340)
OTHER INFORMATION: Wherein Xaa is any
OTHER INFORMATION: specification
US-09-746-491-22
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TITLE OF INVENTION: Novel Proteins and Nucleic Acids
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 200-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SED ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                            ELERVYLRLKPHKAGYQWRFAGSFYFAITVITTIGYGH.VAPS:DGGKVFCMFYALLGIPL 120
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                                                                      ELERLALQAEPHRAGROWKFPGSFYFAITVITTIEYGHAAPGIDSGKVFCMFYALLGIPL 120
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64.3%; Pred. No. 5.2
tive 32; Mismatches
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US-09-431-367B-2
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US-09-336-643-83
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                                                    Sequence 2, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: CUITIS, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-074CP
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GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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SOFTWARE: FastSEQ for
SEQ ID NO 83
LENGTH: 411
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CURRENT APPLICATION NUMBER: US/09/431,367B CURRENT FILING DATE: 1999-11-01 PRIOR APPLICATION NUMBER: 09/259,951
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PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
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CURRENT FILING DATE: 1999-06-18
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ORGANISM: H.
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                                                                                                                                                                                                                                                                                                         MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T
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                                                                                                                                                                                                                                                                                                                                                           FCIIYALLGIPLFGFLLAGVGDQLGTIF-----GKGIAKVEDTFIKWNVSQTKIRI 208
                                                                                                                                                                                                                                                                                                                                                                                 FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD-----VSM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                LIDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                    ISTIIFILFGCVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSD--IEY
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Wang, Jian-Wang
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NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
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SEQ ID NO 8
LENGTH: 313
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Best Local Similarity
Matches 90; Conserv
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Best Local (
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/259,951 PRIOR FILING DATE: 1999-03-01
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                                                                                    TLVMFQSLGERINTLVRYLLHRAKKGLGM-----RRAL
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31.7%; Pred. No. 3.7(
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18 YLLVGAAVFDALESEPELIE-----RQRLELRQQELRAF"...SQGGYEELERVV----- 66
                                                                            YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCY; LDAFVERVLAAG---RLG 73
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                                      DB 5;
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                                                                ANMYLIGFFSCISTLC-- 172
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                                         ACWHLVALLGVVVTVCFL 186
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: H.
US-09-336-643-81
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                                                                                                                   Sequence 5, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: CUITLIS, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES
FILE REFERENCE: MNI-074CP
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SEQ ID NO 81
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Best Local
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                                      CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
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CURRENT FILING DATE: 1999-06-18
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APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
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                       NUMBER OF
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                                                                                                                                                                                                                                                                                                          243 FLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADEDDR 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 RVVLRLKPHKAGVQ---WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                IGAAAFSHYEH-WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQ---YVAFSFVYI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TMLLLTASAQRLSLL---LTHVPLSWLSMRWGWDPRRA----ACWHLVALLGVVVTVCFL 186
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                       SEQ ID NOS: 12
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LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-5
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Best Local S
Matches 81
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LENGTH: 332
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Best Local Similarity
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
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                                                                                 146
                                                                                                                       161 MFLVLTDTGDILATILSTSYNRFRKFPFFTRPLLSKWCF3 FKKKPDPKPADEAVPQII 220
                                                                                                                                                                121
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                                      221 ISAEELPGPKLGTCPSRPSCSMELFERSHALEKQNTLQL: AMERSNSCPELVLGRLSY 280
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Local Similarity 22.9%;
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                                                                                                                                                             TLVMFQSLGERINTLVRYLLHRAKK------
                                                                                                                                                                                                    QGHLQKVKPQWENRTTHWSFLSSLFFCCTVFSTVGYGY (
                                                                                                                                                                                                                                    ERVVLRLKPH--KAGVQWRFAGSFYFAITVITTIGYGH, CETGGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                   LCFLCFLVTYALVGAVVFSALEDGQVLVAADDGEFEKFL;'.'
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Pred. No. 4.7e-15:
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; NUMBER OF SEQ ID NOS: 72 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 63 ; LENGTH: 39 ; TYPE: PRT ; ORGANISM: MUS musculus US-09-746-491-63 ; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 1386 ; LENGTH: 205 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-760-469-1386 Ωy 밁 Qy 밁 ş US-09-760-469-1386, Application US/09760469
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTS54 밁 δÃ 밁 δÃ RESULT 14 US-09-746-491-63 밁 GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids
FILE REFERENCE: 15966-621 Query Match Best Local S Query Match
Best Local Similarity
Matches 34; Conserv Sequence 63, CURRENT APPLICATION NUMBER: US/09/746,491 CURRENT FILING DATE: 2000-12-20 PRIOR APPLICATION NUMBER: USSN 60/171,329 PRIOR FILING DATE: 1999-12-21 CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16 148 GMRRADVSMANMVLIGFFSCISTLCIGAAAFSHYE-HWTEFQAYYYCFITLTTIGFGDYV 206 157 194 FITLTTIGEGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLNLVVLREM 247 256 RDAEH 260 42 EDQVH 161 PGEGYNQKFREL-----YKIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKD 156 A----LQKDQALQTQPQYVAFSFVYILTG----LTVIGAFLNLVVL---RFMTMNAEDEK 255 GFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYV 101 Similarity Application US/09746491 Conservative Conservative 8.8%; 87.2%; 6.68; Score 179; 1 Score 135.5; DB 5; Pred. No. 6e-05; 7; Mismatches 48; Pred. No. 8.9e); Mismatches DB 5; .9e-10; Length 39; Length 205; Indels Indels Encoding 17; 0, Gaps Gaps ن. 0;

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Copyright (c) 1993 - 2000 Comp
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    9 US-09-503-089A-4
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98; Score 2090; DB '); Leng 98; Pred. No. 5.1e- 4; 10; Mismatches Indel 11:11:11:11:11:11:11:11:11:11:11:11:11:	3089A	US-09-432-470-4 US-09-432-470-4 US-09-828-035-2 US-60-258-275-4-4 PCT-US00-34983B-2-2 US-60-212-358-1 US-60-171-487-5-3 US-60-235-25-2 US-09-357-425-1 US-09-357-425-1 US-09-357-425-1 US-09-735-1109-4 US-09-735-1109-4 US-09-735-171-4 US-09-735-171-4 US-09-735-171-4 US-09-735-171-4 US-09-735-171-4 US-09-735-171-4 US-09-735-171-4	-09-655 -09-144 -09-436 -09-852 -09-852 -60-207 -60-216 -60-216 -60-216
ngth 411; els 0; Gaps 0; TIFLVVVLYLII 60	anesthetics	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli	751111111111111111111111111111111111111

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RESULT 2
US-09-828-746-6
; Sequence 6, Applicat.
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.7%;
Best Local Similarity 99.8%;
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PRIOR ETLING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: EP 98300570.3
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
RUMBER OF SEO ID NOS: 6
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CURRENT FILING DATE: 2001-04-09
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                                                                                                                                   LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
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RESULT 4 US-09-336-643-83

Sequence 83, Application US/09336643
GENERAL INFORMATION:
APPLICANT: Miller, Andrew

APPLICANT:

Ping Curran, Mark

APPLICANT:

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APPLICANT: Miller, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Curran, Mark
TITLE OF INVENTION: NOVEL Human Potassium Chan,
FILE REFERENCE: SEQ-15PCT
CURRENT APPLICATION NUMBER: PCT/US99/03826A
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,687
EARLIER FILING DATE: 1998-02-25
EARLIER FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: H. sapiens
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ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHC/ (FDIAVIENMK 411
                                                                  KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDK DEATSVKRKLSAELAGNHNO
                                                                                                                                                                            LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
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Pred. No. 2.6e-195;
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CURRENT FILING DATE: 1999-06-18
EARLIER APPLICATION NUMBER: 60/095,836
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
                                                                                                                                                                                                                  Sequence 83, Application US/09336643A
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
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Best Local S
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SEQ ID NO 83
                                            CURRENT APPLICATION NUMBER: US/09/336,643A CURRENT FILING DATE: 1999-06-18 EARLIER APPLICATION NUMBER: 60/076,687 EARLIER FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 60/116,448 EARLIER FILING DATE: 1999-01-19
                                                                                                                                                      APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium
FILE REFERENCE: SEQ-15P
EARLIER APPLICATION NUMBER: PCT/US99/03826 EARLIER FILING DATE: 1999-02-22 NUMBER OF SEQ ID NOS: 87
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TYPE: PRT
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TITLE OF INVENTION: Novel
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Pred. No. 2.6e-199;
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LENGTH: 411
TYPE: PRT
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SEQ ID NO 83
LENGTH: 411
TYPE: PRT
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                                                          Matches
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Best Local :
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Best Local :
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PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR FILING DATE: 1999-01-25
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Conrad Gerald Chapman TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Helen Jane Meadows APPLICANT: Conrad Gerald Chap
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GEMERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMEY, GEORRES
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identification of anesthetics
FILE REFERENCE: f17b12prov3-humanTREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT FILMS DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
CORMINET: Microsoft Word 2000
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Best Local Similarity 96.1
Matches 395; Conservative
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SEQ ID NO 2
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                                                                                                                                                                                                                                                              97.7%; Score 2041; 96.1%; Pred. No. 5.
                                                                                                                                                                                                                                                 12; Mismatches
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5.2e-199;
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                                                                                                                                                                                                                                                                                                Matches
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FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY_AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Pausch, Mark H.

TITLE OF INVENTION: Potassium Channels, Nu: Gotide Sequences
TITLE OF INVENTION: Encoding Them, and Meth dis of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #10, Version #1.20
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                 SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCII:ALLGIPLFGFLLAGVGDQ 180
                                                         LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCV:.. VALPAVIFKHIEGWSALD 240
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 201-683-2134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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CITY: Parsippany
STATE: New Jersey
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TOPOLOGY: li
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FILING DATE: 11-MAR-1997
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AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGRLVRVIS
                            AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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Encoding Them,
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US-09-655-272-4
; Sequence 4, Application
; GENERAL INFORMATION:
; APPLICANT: HONORE, ERIC
; APPLICANT: FINK, MICHE
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US-08-816-011C-45
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Best Local Sim
Matches 391;
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PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 426
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TITLE OF INVENTION: AND METHODS OF USING S,
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-11
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APPLICANT: Price, Laura &
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APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: DUPRAT, FABRICE
TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
FILE REFERENCE: 1383-00
CURRENT APPLICATION NUMBER: US/09/655,272
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR PILING DATE: 1999-02-23
PRIOR PILING DATE: 1998-03-05
PRIOR APPLICATION NUMBER: FCT/FR99/00404
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
                                                              Sequence 8, Application US/09144914
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
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US-09-144-914-8
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LENGTH: 370
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Best Local Similarity
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OTHER INFORMATION: Description
-09-655-272-4
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                 EARLIER
                               EARLIER APPLICATION NUMBER: 08/749,816 EARLIER FILING DATE: 1996-11-15
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                                                                                                     TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN TITLE OF INVENTION: CLONING AND THEIR USE, TITLE OF INVENTION: DRUGS FILE REFERENCE: 1201-CLT2-00 CURRENT APPLICATION NUMBER: US/09/436,265 CURRENT FILING DATE: 1999-11-08 PRIOR APPLICATION NUMBER: 60/095,234 PRIOR FILING DATE: 1998-08-04 PRIOR FILING DATE: 1998-08-04 PRIOR FILING DATE: 1998-08-04 PRIOR APPLICATION NUMBER: 60/107,692 PRIOR FILING DATE: 1996-11-09 NUMBER OF SEQ ID NOS: 32 SOFTWARE: PATENTIN Ver: 2.1
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                                                                             SEQ ID NO 8
TENGTH: 370
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APPLICANT: DUPRAT, FABRICE
APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: FARMAN, NICOLETTE
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EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
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Best Local Similarity
Matches 366; Conserv
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AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI $ AYFAAVLSMIGDWLRVIS
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SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCI: YALLGIPLEGFLLAGVGDQ 180
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99.5%;
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Pred. No. 4.4e
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ORGANISM: Homo sapiens

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CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
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                                  NUMBER OF SEQ ID NOS: 88 SOFTWARE: PatentIn versions SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Applica GENERAL INFORMATION:
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Best Local
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                                                                                          PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/223,245
PRIOR FILING DATE: 2000-08-04
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TITLE OF INVENTION: Human Ion Channels
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TYPE: PF
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                                                                                                                                                                       APPLICATION NUMBER: 60/216,893 FILING DATE: 2000-07-17
                                                                                                                                                                                                         APPLICATION NUMBER: 60/207,093 FILING DATE: 2000-05-25
                                                                                                                                                   APPLICATION NUMBER: 60/237,873
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99.5%;
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Pred. No. 4.4e-180;
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-852-386-73
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PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR PRIOR PAPLICATION NUMBER: 60/206,526
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR PRIOR DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR PRIOR APPLICATION NUMBER: 60/216,893
PRIOR APPLICATION NUMBER: 60/216,893
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PRIOR APPLICATION NUMBER: 60/217,873
PRIOR APPLICATION NUMBER: 60/2237,873
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                                                                           SEQ ID NO 73
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Best Local Similarity
Matches 247; Conserva
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PRIOR APPLICATION N
PRIOR FILING DATE:
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CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
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APPLICANT: Ruble, Cara L.
TITLE OF INVENTION: Human Ion Channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 00133.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Roberds, Steven L. APPLICANT: Benjamin, Christopher
                                                                                             SOFTWARE:
                                                                                                           NUMBER OF SEQ ID NOS: 88
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                               381 ERRRLGLDQRAHSLDMLSPEKRSV 404
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; ORGANISM: Homo sapiens
US-09-431-367B-2
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local Similarity
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                                                                                                                         APPLICANT: Curtis, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
                   PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
                                                                               CURRENT APPLICATION NUMBER: US/09/431,367B CURRENT FILING DATE: 1999-11-01
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SOFTWARE: PatentIn Ver.
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                                                                                                                                                 MOLECULES
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LENGTH: 332
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; TYPE: PRT
; ORGANISM: Homo
US-09-431-367B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 15
LENGTH: 394
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mu, David
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCMB: A NOV
FILE REFERENCE: 018781-004010US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 NLVVL----NRLGHLMQQGVNHWASRLGGT---WQ-DPDK//SWLAGSGALLSGLLLFLLL 195
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209. ISTIIFILEGCVLEVALPAIIEKHIEGWSALDAIYEVVI!; TTIGEGDYVAGGSD--IEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 YKNGASILSNTTS-MGRWELVGSFFFSVSTITTIGYGHLE; TMAARLFCIFFALVGIPL 143
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                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                       ELDELIQQIVAAINAGIIPLGNTSNQISHNDLGSSFFFA
                                          FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG! "HRRAD-----VSM 156
                                                                               FCIIYALLGIPLFGFLLAGVGDQLGTIF-----GKGIAKVEDTFIKWNVSQTKIRI 208
                                                                                                                          ELERVVLRL-KPHKAGV-----QWRFAGSFYF7
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                                                                                                                                                                                                       MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERCE, LRQQELRARYNLSQGGYE
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31.0%;
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35.9%; Pred. No. 3.20
tive 51; Mismatches
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Pred. No. 1.56'2"
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APPLICANT: Mu, David
APPLICANT: Mularik Inc.
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A Novel Potassium Ch
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR APPLICATION NUMBER: 05 60/186,951
PRIOR FILING DATE: 2000-03-03
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US-09-798-584-1
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PRIOR FILING DATE: 1999-12-21
NUMBER OF SEO ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 60
LENGTH: 365
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60, Application US/09746491
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids
FILE REFERENCE: 15966-621
                                                                                                                                                                                                           Sequence 1, Application US/09798584 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
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CURRENT FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                             274 HISEEARQVRQR 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 YRQLELVILQSEPHRAGV------QWKFAGSFYFAITVITTIGYGHAAPGTDAGK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKW-----NVSQTKIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFCMFYAVLGIPLTLVMFQSLGERM------NTFVRYLLKRIKKCCGMRNTEVS 155
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                                                                                                                                              Query Match
Best Local Similarity
Matches 83; Conserv
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Best Local Similarity
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human KCNB (Potassium Char.e.)
US-09-798-584-1
                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-431-367B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: Curtis, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MC
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 313
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PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
                   335 EEISPSTLKN--SLFPSPISSISPGLHSFTDH 364
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                                                                                 57 YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCV
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LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPL::DAGKAFSIAFALLGVPTTML 136
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                                                                                                                                                              Conservative
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                                                                                                                                                          16.6%; Score 348; DB 34.4%; Pred. No. 2.6e tive 42; Mismatches
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                                                                                                      DELIQQIVAAINAGIIP 116
                                                                             LDAFVERVLAAGRLGRVV 76
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RESULT 9
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US-09-336-643-81
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Sequence 59, Application US/09746491
GENERAL INFORMATION:
APPLICANT: BUTGESS, Catherine E.
TITLE OF INVENTION: Novel Proteins and
FILE REFERENCE: 15966-621
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Best Local Similarity
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PRIOR ETLING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR ETLING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
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CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18
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                     Nucleic Acids
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CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 330
TYPE: PRT
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US-09-746-491-61
Sequence 61, Application US/09746491
GENERAL INFORMATION:
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SEQ ID NO 61
LENGTH: 258
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Best Local Similarity
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Best Local Similarity
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PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
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CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
 109
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                                                                                                                                                                         42 MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTLV1QKQTFISQHSCVNS--T 97
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                                                                                                                                                     1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERGKLELRQLELRARYNLSEGGYE 60
                   FCIIYALLGIPLEGFULAGVGDQLGTIFGKGIAKVEDTETKWNVSQTK-----IRI 208
                                                                       ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
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ELERVVLRL-KPHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV 108
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FCMFYALLGIPLTLVMFQSLGERI------NTFVRYLLHRAKRGLGMRHAEVSM 156
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hilarity 34.9%;
Conservative 4;
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                                                                                                                                                                                                                            16.3%; Score 342.5; DB 5; 30.0%; Pred. No. 6.3e-24; tive 61; Mismatches 54;
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Pred. No. 3.1e-24;
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CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 330
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Sequence 58, Application US/09746491
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids; FILE REFERENCE: 15966-621
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          NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 22
LENGTH: 393
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                   Sequence 22, Application US/09746491 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                     FILE REFERENCE: 15966-621

CURRENT APPLICATION NUMBER: US/09/746,491

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: USSN 60/171,329

PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                             APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 ANMVLIGEVSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT 216
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Pred. No. 1.7e-23;
12; Mismatches 96;
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; NAME/KEY: VARIANT; COCATION: (340)
; COCATION: (340)
; OTHER INFORMATION: Wherein Xaa is any amino; OTHER INFORMATION: specification
US-09-746-491-22
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Best Local Similarity
Watches 77; Conserve
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-11
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APPLICANT: CUITLIS, ROY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 11
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CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12
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                               210
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                               KPADEAVPQIIISAEELPGPKLGTCPSRPSCSMELFERSHALEKQNTLQLPPQAMERSNS 269
                                                                                               CMLYALFGIPLMFLVLTDTGDILATILSTSYNRFRKFPF: FRPLLSKWCPKSLFKKKPDP
                                                                                                                                                           ETVVEDRKQDLQGHLQKVKPQWFNRTTHWSFLSSLFFCcccccStVGYGYIYPVTRLGKYL 149
                                                                                                                                                                                                                          LVTYALVGAVVFSAIE------DGQVLVA---
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 -NVSQT---
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Pred. No. 4.6e-11;
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-KIRIISTIIF1LFGCVLFVALPAIIFKHIEG
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                                                                                                                                                                                                                                                                                                                      Length 401;
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US-09-760-469-1386
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; ORGANISM: H.
US-09-336-643-16
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US-09-336-643-16
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                                                                               Sequence 1386, Application US/09760469
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16 LENGTH: 197
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983
                                             CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edw
APPLICANT: Hu, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US99/03826 PRIOR FILING DATE: 1999-02-22
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TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                              160 RPSGPVTAE 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 IISTIIFILFGCVLFVALPAIIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAG-GSDIE 265
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                                                                                                                                                                                                                                                                                                                                                         -----PVIYHLGQLALLGYLLLGL-----LAML-----LAVETFSELPQVRAMGKFF 159
                                                                                                                                                                                                                                                                                                                                                                                                                                         LLQAVALGLIVASSFVLLPALVLWGLQGDCSLLGAVYFCFSSLSTIGLEDLLPGRGRSLH 117
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GENERAL INFORMATION:
APPLICANT: CUITIS, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
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SEQ ID NO 2
LENGTH: 499
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CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                    CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                                                                                                       APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES
FILE REFERENCE: MNI-074CP
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SOFTWARE:
                   NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAITGNOT--FUNWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPL---C 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLAW----LSLF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI 233
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                                                                                                                                                                                                                                                                                                                                                                                           ---VEVHKAIKKRRRR--
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; Sequence 15, Application US/09798584
(GENERAL INFORMATION:
APPLICANT: M., David
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KONB: A Novel Potassium (**... el
FILE REFERENCE: 018781-004010US
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US/09/186,951
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-5
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Best Local Similarity
Matches 88; Conserv
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LENGTH: 332
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LENGTH: 394
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                   109
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                                                                       158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 NLVVL----NRLGHLMQQGVNHWASRLGGT---WQ-DPDK# * *LAGSGALLSGLLLFLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 INAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGN1: ECGKIFCIIYALLGIPL 169
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                                                                                                                                                                                                 42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQR: X-VIOKOTFIACHACVNS--T 97
                                                                                                                                                                                                                                                                        Local Similarity
                               ELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGSSFFFA VITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYVIGMNDSQRYPLWYKNWVSLWILFGMAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAAVLSMI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAVIFKHIEGWSALDAIYFVVITLTTIGEGDYVAGGSDIE: | DFYKPVVWFWILVGLAY 284
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ISTIIFILFGCVLFVALPAVIFKHIEGWSALDAIYFVVITL!T1GFGDYVAGGSD--IEY
                                                                                                                                                                                MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERCT:.ELROQELRARYNLSQGGYE
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35.5%;
                                                                                                                                                                                                                                                                     17.7%; Score 370; DB : Length 394; 28.0%; Pred. No. 1.4e--/5;
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Pred. No. 2.9e-2:
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Gaps

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RESULT 6
US-09-746-491-60
; Sequence 60, Application US/09746491
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 59
LENGTH: 330
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GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding
FILE REFERENCE: 15966-621
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Best Local Similarity
                CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
                                                                                                APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Novel Proteins and Nucleic FILE REFERENCE: 15966-621
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                           175 AVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-EALQRKLPYVAFSFLYILLGLT 233
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                                                                                                                                                                                                                                                                                234 VIGAFLNLVVLRFLVASADW 253
                                                                                                                                                                                                                                                                                                                   284 YFAAVLSMI-----GDW 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --INAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGI 167
                                                                                                                                                                                                                                                                                                                                                                                                AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF----WILVGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                        PLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE----NLVVAGLLACAATLALG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLEGELLAGVGDQLGTIFGKGIAKVEDTE-IKWNVSQTKIRIISTIIFILEGCVLEVALP 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%; Score 351.5; DB 5; 35.0%; Pred. No. 5.7e-25; vative 44; Mismatches 94;
                                                                                                                   Acids
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US-09-746-491-60
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SEQ ID NO 60
LENCTH: 365
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LENGTH: 258
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Best Local Similarity
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Matches 94; Conserv
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CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Novel Proteins and Nucleic Acids FILE REFERENCE: 15966-621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 KVFCMFYALLGIPLTLVMFQSLGERI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 IISTIIFILFGCVLFVALPAVIFKHIEGWSALDAIYFVVITHTIIGFGDYVAGGSD--IE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AFCMFYAVLGIPLTLVMFQSLGERM------NIFV *.LLKRIKKCCGMRNTEVS 155
                                                        156 KIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDIFIKWNVSQTK------I 206
                                                                                                                                   100 D-ELIQQIVAAI---NAGIIPLGNSSNQVSHWDLGSSFFFRAC VITTIGFGNISPRTEGG 155
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                                                                                                58 GYEELERVVLRLKPHKAGV
                                                                                                                                                                                                                 42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIV OKOTFIAQHACVNSTEL 99
                                                                                                                                                                           1 MKKQNVRTLSLIACTFTYLLVGAAVFDALESDHEMREE: : KAEEIRIRGKYNI--STED 58
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                                                                                                                                                                                                                                                                           16.8%; Score 350.5; 14' 31.2%; Pred. No. 5e-25;
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US-09-746-491-58
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 330
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 15966-621
                                                                                                           NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09746491 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Novel Proteins and Nucleic FILE REFERENCE: 15966-621
                                                                                                                                                                                 PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: USSN 60/171,329
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
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CURRENT FILING DATE: 2000-12-20
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NAME/KEY: VARIANT
                                          ORGANISM: Homo sapiens
                                                                   TYPE: PRT
                       FEATURE
                                                                                        LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --INAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF---WILVGLA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE----NLVVAGLLACAATLALG
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APPLICANY: Powers, Scott
APPLICANY: Tularik Inc.
TITLE OF INVENTION: KCNB: A Novel Potassium (FILE REFERENCE: 018781-004010US)
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: human KCNB (Potassium Channel US-09-798-584-1
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                                                                                                                                                                                                                                                                                                                         Matches 104;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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109
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                                                                                                                                                  RQLELVILQSEPHRAGV-----QWKFAGSFYF7: "VITTIGYGHAAPGTDAGKA 108
                                                                 FCMFYAVLGIPLTLVMFQSLGERM------NTFVRY LKRIKKCCGMRNTDVSM 156
                                                                                                      FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKW-----NVSQTKIRI 208
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                                                                                                                                                                                                                                                                                                                                           16.4%; Score 342.5; DB 5; 26.5%; Pred. No. 4.7e-21;
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; TYPE: PRT ; ORGANISM: Homo sapiens US-09-431-367B-8
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GENERAL INFORMATION:
APPLICANT: CURTLIS, RORY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
FILE REFERENCE: MNI-074CP
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Best Local Similarity
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LENGTH: 313
                                                                                                                                                                                                                        Sequence 81, Application US/09336643 GENERAL INFORMATION:
                                                             APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15¢
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-09-431-367B-8
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PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
              CURRENT APPLICATION NUMBER: US/09/336,643 CURRENT FILING DATE: 1999-06-18
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SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVA--LPAVIF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 KIEEISPSTLKNSLFPSPISSISPGLHSFTDH 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 VTAEFKETRRRLSVEI------YDKFQRATSVKRKLSAELAGNHNQELTPCR 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAMVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 KPLYVAFSFMYILVGLTVIGAFLNLV--VLRFLTMNSEDERRDAEERASLAGNRNSMVIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGNSSNQVS----HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTLSVNHLTSEREVLPPLLKAESIYLNGLTPH 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVV 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPEEPRPSRPRYKADVPDLQSVCSCTCYRSQDYGGRSVAPQNSFSAKLAPHYFHSIS-•Y 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 342; DB 5; Length 313; Pred. No. 4e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104;
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; TYPE: PRT
; ORGANISM: H.
US-09-336-643-81
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, Sequence 11, Application US/0; GENERAL INFORMATION:
, APPLICANT: Curtis, Rory A.J.
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                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/259,951 PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/431,367B CURRENT FILING DATE: 1999-11-01
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PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL FILE REFERENCE: MNI-074CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 401
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                                                                                                                                                                                                                                      Y match 10.1%; Score 212; DB Local Similarity 20.8%; Pred. No. 6.7e-... les 77; Conservative 37. Minmath
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                                                             90 ETVVEDRKQDLQGHLQKVKPQWFNRTTHWSFLSSLFFCCT3.
                                                                                                                                                                                            54 VYLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHA: 1:TELDELIQQIVAAINAG 113
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                                                                                                                                                        47 LVTYALVGAVVFSAIEDGQVL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn
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                                                                                                           ----NQVSHWDLGSSFFFAG
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'LFGCVLFVA--LPAVIF 230

PETIQQIVAAINAGIIP 116 DAFVERVLAAGRLGRVV 76

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Length 313;

\LLGVVVTVCFLVPAVIF 192 *APVVWFWILVGLAYFAAV*

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STVGYSYIYPVTRLGKYL 149

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RESULT 15
US-09-760-469-1386
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:
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SEQ ID NO 16
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.3%; Score 152.5; DB 5; Best Local Similarity 27.5%; Pred. No. 8.1e-07; Matches 52; Conservative 39; Mismatches 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 RPSGPVTAE 168
                                                                                                                                                                       318 -- TANVTAE 324
                                                                                                                                                                                                                                                                                                                                      208 IISTIIFILFGCVLFVALPAVIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAG-GSDIE 265
                                                                                                                                                                                                                                                                                                                                                                                                                          148 ISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIR 207
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                                                                                                                                                                                                                                                         266 YLDFYKPVVWF-----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEW 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 CPELVLGRLSYSIISNLDEVGQQVERLDIPLPIIALIVFAYISCAAAI-LPF----- 320
                                                                                                                                                                                                                                                                                                   58 LLQAVALGLLVASSFVLLPALVLWGLQGDCSLLGAVYFCFSSLSTIGLEDLLPGRGRSLH 117
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                                                                                                                                                                                                                                                                                                                                                                                  MAPLSPGGKAFCMVYAALGLPASLALVATLRHCLLPVLSRPRAWVA----VHWQLSPARAA 57
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Rutter, Marc
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1386
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1386
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Best Local Similarity
Matches 39; Conserv
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ54
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - consult PALM \phi_{\rm c} file wrapper NUMBER OF SEQ ID NOS: 1983
156 DEDQVHIIE 164
                                                                                                                                                                                                               197 IKWNVSQTKIRIISTII--FILFGCVLFVALPAVIFKI
                                          308 GEFRAHAAE 316
                                                                                                                          254 FGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSWIGDWLRVISK-----KTKEEV 307
                                                                                  97 LGDYVPGEGYNQKFRELYKIGITCYLLLGLIAMLVVLET CE-LHELKKFRKMFYVKKDK 155
                                                                                                                                                                     39 IRWGFSKQVVAIVHAVLLGFVTVSCFFFI--PAAVFSVL DDWNFLESFYFCFISLSTIG 96
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                            7.2%; Score 151; DB 3; 30.2%; Pred. No. 1.2e_15
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Search completed: August 28, 2001, 17:11:45 Job time: 389 sec

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US-09-828-746-6	US-08-816-011C-45	US-08-816-011A-45	US-09-828-746-2	US-09-336-643-83	US-09-336-643-83	PCT-US99-03826-83	US-09-503-089A-2	ID
sequence 6, Appli	Sequence 45, Appl	sequence 45, Appl Sequence 45, Appl	Sequence 2, Appli	Sequence 83, Appl	Sequence 83, Appl	Sequence 83, Appl	Sequence 2, Appli	Description

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803 803 776.5 759.5 759.5 759.5 1519 519 427 427 427 427 427 427 427 427	1833 1824 1824 1243 1243 1241.5 1205 1205 1205 1803 803 803 803
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US-60-258-275-3 W US-09-729-739-1 W US-09-655-272-2 W US-09-655-272-2 W US-60-212-358-1 W US-60-229-525-3 W US-60-229-525-3 W US-60-212-358-1 W US-60-212-358-1 W US-60-171-487-5 W US-60-171-487-5 W US-60-223-269-8 W US-60-223-269-8 W US-09-259-951-2 W US-09-259-951-2 W US-09-357-425-6 W US-09-357-425-6 W US-09-35-169-4 W US-09-735-169-4 US-09-735-171-2 US-09-735-171-2 US-09-735-171-4 US-09-735-171A-2	-09-655 -09-144 -09-436 -09-852 -09-852 -60-216 -60-236 -60-236 -09-729 -09-432 -09-432
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ALIGNMENTS

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61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTEL V:LIQQIVAAINAGIIPLGNT 120	61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTEL ::JQQIVAAINAGIIPLGNT 120	1 MAAPDILIDPKSAAQNSKPRISFSTKPTVLASRVESDTTI KKWKTVSTIFIVVVLYLII 60 	Query Match 100.0%; Score 2100; D. 19; Length 411; Best Local Similarity 100.0%; Pred. No. 1.6: .03; Matches 411; Conservative 0; Mismatches D: Indels 0; Gaps	RESULT 1 US-09-503-089A-2 Sequence 2, Application US/09503089A GENERAL INFORMATION: ANANDA J. APPLICANT: HONORE, ERIC APPLICANT: LESAGE, FLORIAN APPLICANT: LESAGE, FLORIAN APPLICANT: LADUSKI, MICHEL TITLE OF INVENTION: A method for the identification of anesthetics FILE REFERENCE: f17b12prov3-humanTREK CURRENT APPLICATION UNMER: US/09/503,089A CURRENT FILING DATE: 2000-02-11 NUMBER OF SEQ ID NOS: 5 SOFTMARE: Microsoft Word 2000 SEQ ID NO 2 LENGTH: 411 TYPE: PRT ORGANISM: Homo sapiens US-09-503-089A-2

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Best Local Similarity
Matches 410; Conserv
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 83
LENGTH: 411
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ORGANISM: H. s
T-US99-03826-83
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EARLIER FILING DATE: 1998-02-25
EARLIER APPLICATION NUMBER: 60/095,836
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Novel Human Potassium Channels FILE REFERENCE: SEQ-15PCT
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Pred. No. 5.2e
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APPLICANT: Miller, Andrew
APPLICANT: Curran, Mark
APPLICANT: Curran, Mark
APPLICANT: Ping Hu
APPLICANT: Marc Rutter
APPLICANT: Marc Rutter
APPLICANT: Marc Rutter
APPLICANT: Marc Rutter
APPLICANTON: NOVel Human Potassium Che
FILE REFERENCE: SEO-15p
CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-6-18
EARLIER APPLICATION NUMBER: 60/095,836
EARLIER FILING DATE: 1998-08-07
EARLIER FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 83
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Best Local :
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RESULT 4
US-09-336-643-83
: Sequence 83, Application US/09336643A
; GENERAL INFORMATION:

APPLICANT: Miller, Andrew

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CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: EP 98300570.3
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 6
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ORGANISM: H.
S-09-336-643-83
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Best Local
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                                                                                                                                                          APPLICANT: Helen Jane Meadows
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-D1
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EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEO ID NOS: 87
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APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
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Pred. No. 5
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nes 0;
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; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO 9
US-09-828-746-2
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US-08-816-011-45
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Best Local S
Matches 410
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GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
SEQ ID NO 2
        REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                          APPLICATION NUMBER: US/08
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Potassium Chan TITLE OF INVENTION: Encoding Them,
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                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
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TELEPHONE:
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nes 410; Conserv
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One Campus Drive
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Encoding Them, and M
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                                ,421-C2
                                                                                                                                                              Version
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 426 amino acids

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                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011A
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,421-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 45, Application US/08816011A GENERAL INFORMATION:
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Best Local
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APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Potass
TITLE OF INVENTION: Encodi
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
TELECOMMUNICATION INFORMATION: TELEPHONE: 201-683-2134
                                                                                                                                                                                                                                                                                                   STREET: One Campus
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
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STRANDEDNESS: single
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Pred. No. 1.
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l.2e-199;
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1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTinVMKWKTVSTIFLVVVLYLII 60

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TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEC INTITLE OF INVENTION: AND METHODS OF USING SAME FILLE REFERENCE: 01142.0122 SEQUENCE LISTING CURRENT APPLICATION NUMBER: US/08/816.011C CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332.312
PRIOR APPLICATION NUMBER: 08/332.312
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
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                                                                                 US-08-816-011C-45
                                                                                                                            SOFTWARE: PatentIn Ver.
SEQ ID NO 45
LENGTH: 426
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
               Query Match
Best Local
 Matches
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                                                                                                                                                            NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 201-683-4117 INFORMATION FOR SEQ ID NO:
                                                                                               ORGANISM: Homo sapiens
                                                                                                                 TYPE: PRT
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Local Similarity
les 405; Conserv
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TYPE: amino acid
STRANDEDNESS: single
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             Score 2062; Db 12;
Pred. No. 1.2e-179;
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                                  Db 12;
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US-09-503-089A-4
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TITLE OF INVENTION: A method for the identification
FILE REFERENCE: £17b12prov3-humanTREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 4
LENGTH: 411
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Best Loc
Matches
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GENERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMEY, GEORGES
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hes 395;
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AIYEVVITLTTIGEGDYVAGGSDIEYLDEYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
                                           SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
                                                                                                                                          GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
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                                                                                                                                                                                                                                97.2%; Score 2041; DB 19; Length 96.1%; Pred. No. 1.6e-197;
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APPLICANT: Central Officers of Applicant: Helen Jane Meadows
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-D1
CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR FILING DATE: 1999-01-25
PRIOR FILING DATE: 1999-01-25
PRIOR FILING DATE: 1998-01-27
PRIOR FILING DATE: 1998-10-7
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 6
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 411
TYPE: PAT
ORGANISM: HOMO SAPIENS
US-09-828-746-6
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US-09-828-746-6
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Best Local Simi
Matches 394;
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SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC (YALLGIPLFGFLLAGVGDQ 180
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94; Conservative
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95.9%; Pred. No. 6.3e ...
tive 12; Mismatches ...
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                                             RATSVKRKLSAELAGNHNQ
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US-09-655-272-4

Sequence 4, Application US/09655272
GENERAL INFORMATION:
APPLICANT: HONORE, ERIC
APPLICANT: FINK, MICHEL

No. 1

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US-09-144-914-8
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NUMBER OF SEO ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 4
LENGTH: 370
TYPE: PRT
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                                                                                                                                                                                                                  Sequence 8, Application US/09144914 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                             APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
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TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: ACTIVATABLE BY POLYUNATURATED FATTY ACIDS AN
TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
FILE REFERENCE: 1383-00
CURRENT APPLICATION NUMBER: US/09/655,272
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR APPLICATION NUMBER: FR 98/02725
PRIOR APPLICATION NUMBER: FR 98/02725
                                                                                           TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS FILE REFERENCE: 989.6705CIP
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
                                                       CURRENT APPLICATION NUMBER: US/09/144,914 CURRENT FILING DATE: 1998-09-01
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96.7%;
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Pred. No. 1.7e-176;
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                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 370
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GENERAL INFORMATION:
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Best Local Similarity
Matches 355; Conserv
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LENGTH: 370
                                                                                  TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF TITLE OF INVENTION: DRUGS
FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1996-08-04
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-13-09
PRIOR FILING DATE: 1996-13-09
PRIOR FILING DATE: 1996-13-09
PRIOR SEGUID NOS: 32
                                                                                                                                                                                                                                                                   APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: FARWAN, NICOLETTE
APPLICANT: LAZDUNSKI, MICHEL
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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EARLIER APPLICATION NUMBER: FR 96/01565
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ORGANISM: Murine
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96.5%;
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Pred. No. 1.3e-175;
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CURRENT APPLICATION NUMBER: PCT/US01/14965
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-05
PRIOR PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/216,893
PRIOR PRIOR APPLICATION NUMBER: 60/237,873
PRIOR APPLICATION NUMBER: 60/237,873
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PCT-US01-14965-73
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; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-436-265-8
: NUMBER OF SEQ ID NOS: 88
: SOFTWARE: PatentIn version
: SEQ ID NO 73
: SEQ ID NO 73
: LENGTH: 543
: TYPE: PRT
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Best Local Similarity
Matches 355; Conserv
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TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.PCT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Roberds, Steven L.
APPLICANT: Benjamin, Christopher
                                                                                      PRIOR APPLICATION NUMBER: 60/223,245 PRIOR FILING DATE: 2000-08-04
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96.5%;
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Pred. No. 1.3e-175;
8; Mismatches 5;
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                                                                    PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR PPLICATION NUMBER: 60/206,526
PRIOR PPLICATION NUMBER: 60/207,033
PRIOR PPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/2016,893
PRIOR PILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/233,245
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Roberds, Steven L.
APPLICANT: Benjamin, Christopher
APPLICANT: Karnovsky, Alla M.
APPLICANT: Ruble, Cara L.
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.US1
CURRENT APPLICATION NUMBER: US/09/852,386
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
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Best Local Similarity 62.7%;
Matches 247; Conservative
                    SOFTWARE: Patentin
SEQ ID NO 73
                                                       NUMBER OF SEQ ID NOS: 88
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
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62.7%;
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                                379 -SME------RRRLGLDQRAHSLDMLSP 399
                                                                   350 LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
                                                                                                                                                                        22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
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Search completed: August 28, 2001, 17:11:13 Job time: $602\ \text{sec}$

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Total number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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US-08-677-734A-11
US-08-677-734A-12
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US-08-953-023A-5
US-08-953-023A-5
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US-09-326-012-4
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-09-236-080-2
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US-09-236-080-2
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Patent No. 6242217
GENERAL INFORMATION:
APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-08-953-139B-

US-08-956-242-

US-09-351-215-4

US-09-351-215-4

US-08-637-823B-1

    Mismatches

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Pred. No. 5e-2.
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                                                                                                                                                                                                                 Sequence 4, Application US/09236080 Patent No. 6242217 GENERAL INFORMATION:
                               NUMBER OF SEO ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
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Best Local :
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
                                                                                                         CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25
                                                                                                                                             TITLE OF INVENTION: NO. FILE REFERENCE: GP30031
                                                                                                                                                                              APPLICANT: Helen Meadows APPLICANT: Conrad Chapman
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ORGANISM: Homo sapiens
                    TYPE: PRT
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95.98;
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Pred. No. 6.9e-200;
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APPLICANT: Lesage
                                                                                                                                                                                                                                  TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08,
FILING DATE: 15-NOV-196
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BARHAILD, JACQUES
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
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                            51 FLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFIS HSCVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version 4
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                                                                                                                                                                                                                                                                                                          NAME: Weiser, Gerard J
REGISTRATION NUMBER: 19
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                                                                                                                                                                      TOPOLOGY:
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Patent No. 5559026
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Price, Laura A. APPLICANT: Pausch, Mark H.
     129
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                                 166 GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-----QTKIRIISTIIFILF-G 218
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                                                                     69
                                                                                                                                                                50 IFLVVVLYLIIGATVFKALEQPHE----ISQRTTIVIQKQTFISQHSCVNSTELDELIQQ 105
                                                                                                                                                                                                                                                                                                                                        LENGTH: 618 amino acids
TYPE: amino acid
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                                                                                                                                    LLIFYISYLMFGAAIYYHIEHGEEKISRAEORKAQIAINEYLLEELGDKNTTTQDEILQR 68
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                                                                   ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI 128
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-LGEYFGRTFEAIYRRYKKYKMSTDMHYVPPQLGLITTVVIALIPG
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Pred. No. 2.8e-21;
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US-08-332-312-4
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Patent No. 5559026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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STREET: U.
STREET: Wayne
                                                                     132 RI----PAFLVLAILIVYTAFGGVLMSKLEPWSFFTSFYEGFITMTTVGFGDLMPRRDGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 TAEFKETRRRLSVEIY 337
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                                                                                                                                   205 KIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALDAIY COTTLTTIGFGDYVAGGSDI 264
                                                                                                                                                                                                                                                                   120 TSNQISH-----WDLGSSFFFAGTVITTIGFGNISPRILLSIFCIIYALLGIPLFGFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 TKDVGYLRRMLN-ELY 311
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Harrington, James REGISTRATION NUMBER: P-
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                                                                                                                                                                                                                                                                                                                                     TSNEVKKNAATETWTFSSSIFFAVTVVTTIGYGNPVPVTNIGRIWCILFSLLGIPL---T 71
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Pausch, Mark H.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
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NAME: Welser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/749,816 FILING DATE: 15-NOV-1996
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                                                                                                                                            ITSGIENSEQSIEIYTKKLILMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVI 148
                                W----NVSQTKIRIISTIIFILFGCVLFVALPAI---IFKHIEGWSALDAIYFVVITLTT 251
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230 South Fifteenth Street, Suite 500
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Fink, Michel
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Lazdunki, Michel
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24.3%;
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Pred. No. 4.4e-10;
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US-08-749-816-3
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Best Local Similarity
Matches 58; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
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151 IAFKFEFGTFLAHF---LVVVSNRTRLAVKKAYYKLSQNFENAETPSNSLQHDYLIFLSS: 207
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                                                                   94 S---KLGKCLTKSSRIDGFGKAIFFSWTLYSTVGYGSLYPHSTLGRYLTIFYSLLMIPVF 150
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                                                                                                                                                                      52 LVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISCOSCVNSTELDELIQQIVAAIN 111
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REGISTRATION NUMBER: 1
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Lazdunki, Michel
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US-09-135-021-2
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Best Local
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APPLICANT: Keating, Mark T.
APPLICANT: Reating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
FILE REFERENCE: 2323-128
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT FILING DATE: 1980-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
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KKSVVVKKK----KFKLDKDNGVTPGEKMLTVPHITCD----PP
                                     QRATSIKRKLSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
                                                                          QQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSSTWKIYIR---KAPRSHTLLSPSPKP
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                                                                                                                                                      TVTTIGYGDKV------PQTWVGKTIASCFSVFAISEFALPAGILGSGFALKV
                                                                                                                                                                                                                                                                         RIISTIIFI---LFGCVLFVALPAIIFK-------HIEGWSALDAIYFVVI
                                                                                                                                                                                                                                                                                                              ----SKGQVFA-TSAIRGIRFLQILRMLHVDRQGGT--
                                                                                                                                                                                                                                                                                                                                                                                             FFG----TEYVVRLWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVASMVVLCVG---
                                                                                                                                                                                                                                    RLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVV
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                                                                                                                 -----FRAHAAE-----WTANVTAEFKETRRRLSVEIYDKF 340
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RESULT

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ADDRESSEE:

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US-08-677-734A-11
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; ORGANISM: Homo
US-09-135-021-80
                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                               Description US/08677734A Patent No. 5871919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-13, Sequence 80, Appr. Sequence 80, Appr. No. 6150104
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APPLICANT: Keating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN A HICH CAUSES JERVELL
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROM:
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT FILING DATE: 1998-08-17
CURRENT FILING DATE: 1998-08-17
                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Brant, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILLING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 80 SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 581
                                  APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distril',
TITLE OF INVENTION: Functional Analysis Of,
TITLE OF INVENTION: NHE3.
                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                     308
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                   HTLLSPSPKPKKSVVVKKK---KFKLDKDNGVTPGEKMLTVPHITCD----PP
                                                                                                                                                                                                                                                                                                                                                      RLSVEIYDKFQRATSIKRKLSAELAGNHNQELTPCRET VEHLTNERDVLPP 383
                                                                                                                                                                                                                                                                                                                                                                                                                         MIGDW--LRVISKKTKEEVGE------FRAHAA...----WTANVTAEFKETRR 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----EIVLVVFFG-----TEYVVRLWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVAS 114
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Finnegan, Henderson, Farabow, Garrett &
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20005-3315

Washington

1300 I Street,

Suite

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US-08-677-734A-9
; Sequence 9, Application US/08677734A
; Patent No. 5871919
; GENERAL INFORMATION:
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Best Local Similarity
Tatches 76; Conserve
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                                  APPLICANT:
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                     305 AILAITFCGICCQKYVKANISEQSATTVRYTMKMLASGAET 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                             KGIVSFFVVSLGGTLVGV-IFAFLLSLVTRFTKHVRIIEPGFVFVISYLSYLTSEMLSLS 304
                                                                                                                                                                                                                                                                                                                  KPVVWFWI-----LVGLAYFAAVLSMIGDW---LRVI-----
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                                                                                                                                                                                                                                                                                                                                                                                         -----IIFKHIEGWSALD-----AIYFVVITLTTIGFGDYVAGGSDIEYLDFY 270
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Fordis, Jean B.
Fordis, Jean B.
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                                Brant, Steven R
Yun, Chris C.H.
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                 Donowitz, Mark
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Chung-Ming
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19.08;
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APPLICANT:

Steven

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US-08-677-734A-10
; Sequence 10, Application US/08677734A
; Patent No. 5871919
; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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NAME: Fordis, Jean B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1:
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                                                                                                                                                                                                                                                                                                                                            152 TEGGKIFCIIYALL------GIPLFGFLLAG-VGD-(_;----TIFGKGIAKVEDTF 196
                                                                                                                        292 IISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISECS YTTVRYTMKMLASSAET 348
                                                                                                                                                                                                                                                                                                                                                                                           90
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CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 KWKTVSTIFLVVVLYLIIGATVFKALEQPHEISQRTTIV! COTFISQHSCVNSTELDEL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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                                                                                                                                                                                                                                                                                         IKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSAL-DAIYFVVITLTTIGFG
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                                                                                                                                                                                                                                                        ------PVAVLAVFEEVHVNEVLFI----IVF----CFSLLNDAVTVVLYNV----FE 232
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20005-3315
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99.5; Dagg.
Pred. No. 0.19; %
                                                                                                                                                        --SKKTKEEVGEFRAHAAEWTANVTAEFKET
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US-08-677-734A-12 ; Sequence 12, Application US/08677734A
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fordis, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
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LENGTH: 834 amino acid
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TITLE OF INVENTION: Funct
TITLE OF INVENTION: NHE3.
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 IQQIVAAINAGIIPLGNTSNQISHWDLGSSFFF-----AGTVI-TTIGFGNISPR 151
                                                                                                                                                                                                                                                                                                                                                                                         152 TEGGKIFCIIYALL------GIPLFGFLLAG-VGD-QLG----TIFGKGIAKVEDTF 196
                                                                                                      292 IISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISEQSATTVRYTMKMLASSAET
                                                                                                                                                                                 233 SFVALGGDNVTGVDCVKGIVSFFVVSLGGTLVGVV-FAFLLSLVTRFTKHVRIIEPGFVF
                                                                                                                                                                                                                           256 DYVA-GGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMIGDW---LRVI----- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                    90 ---VLGLVLGGIV---WAADHIASETLTPTVFFFYLLPPIVLDAGYFMPNRLFFGNL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 KWKTVSTIFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDEL 102
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                          IKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSAL-DAIYFVVITLTTIGFG 255
                                                                                                                                                                                                                                                                                                                                                   ---GTI--LLYAVVGTVWNAATTGLSLYGVFLSGLMGDLQIGLLDFLLFGSLMAAVD---
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                                                                                                                                                                                                                                                                    ----PVAVLAVFEEVHVNEVLFI----IVF----GESLLNDAVTVVLYNV----FE 232
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Pred. No. 0.19;
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                                                                                                                                            SKKTKEEVGEFRAHAAEWTANVTAEFKET 328
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                   139 L----GSI--LLYAVVGTVWNAATTGLSLYGVFLSGI---
                                                                    295 W---LRVI----
                                                                                                      225 VLYNVFQSFVTLG-GDKVTG-----VDCVKGIVSFFVV.
                                                                                                                                  241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI
                                                                                                                                                                                                              199 WNVSQTKIRIISTIIFILFGCVLFVALPA-----
318 TANVTAEFKET 328
                                                                                                                                                                                                                                                                                  148 ISPRTEGGKIFCIIYALL------GIPLFGFLLAGVGDOLGTIFGKGIAKVEDTFIK 198
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CITY: Washington
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                                 FTKHVRVIEPGFVFIISYLSYLTSEMLSLSSILAITFCG (*
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Chris C.H.
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19.7%; Pred. No. 0.31;
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7; Mismatches
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al Analysis Of the Human Na+/H+ Exchanger Isoform,
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                                                                                                        "STLVGVV-FAFLLSLVTR 276
                                 PRYVKANISEQSATTVRY
                                                                  SKKTKEEVGEFRAHAAEW 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 832;
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337 TMKMLASGAET 347

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; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1036 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-720-484A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SVOIDODA, CTAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: VENUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             396
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                       282 LAYFAAVLSMIGDWLRVISKKT-KEEVGEFRAHAAEWTANVTAEFK--ETRRRLSVEIYD 338
                                                                           502 EW-AOSFROFIICKISSV-FEEKSSCRIENRPSVGVLQLHLLCLFSSGIVMSTWCW----
                                                                                                                                                                                                        189
                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                               101 ELIQQIVAA---INAGII-------PLGNTSNQISHWDLGSSFFFAG-----TV 139
                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                                                                                             446 MVMLFGLKHFANDIKSTSASNKIHLIIMRMGVCALLTLVFIL----VAIACHVTEFRHAD
                                                                                                                                                                                                                                                                                                                           338 SCIVIFVLVYYFLTAGMVWFVFLTYAWHWRAMGHVQDRID--KKGSYFHLVAWSLPLVLT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                               44 WKTVSTIFLVVVLYL---IIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELD 100
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                                                                                                                   GWSALDAIYFVVITLTTIGFGDYVA------GGSDIEYLDFYKPVV----WFWILVG
                                                                                                                                                                                                                                                                ITTIGFGNISPRTEGGKIFCIIYA------LLGIPLFGFLLAGVGDQLGTIFGKG 188
-----TPSSIETWKRYIRKKCGKEVVEEVKMPKHKVIAQTWAKRKDFEDKGRLSITLY- 608
                                                                                                                                                                                                   IA-----KVEDTFIKWNVSQTKIRII------STIIFILFGCVLFVALPAIIFKHIE 234
                                                                                                                                                                                                                                           ITTMAFSEV----DGNSIVGICFVGYINHSMRAGLLLG-PLCGVILIG-----GYFITRG
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650/952-9881
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Rosenthal, Arnon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 96.5; DB 2;
21.8%; Pred. No. 0.54;
ative 53; Mismatches 154;
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25;

	641 PQCVKRRMAL 650	641	Db
	395 LTPHCAGEEIAV 406	395	Qy .
640	•	609	Db
39,	339 KFQRATSIKRKLSAELAGNHNQELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNG 39.	339	Qy

Search completed: August 28, 2001, 17:06:21 Job time: 525 sec

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Minimum
Maximum
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Listing first 45 summaries
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Perfect score:
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seg length: 2000000000
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Gapop 10.0 ,
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2100
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(SIDSB/gcgdata/geneseq/yeneseqp/AA1389.DAT:*

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Copyright (c) 1993 - 2000 Comp
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/SIDSB/gcgdata/geneseq/geneseqp/AA1987.DAT:*
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                                                                                                                                                                                                                                                                        SUMMARIES
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	139.5	139.5	140.5	140.5	140.5	147.5	147.5	147.5	147.5	153.5	160.5	166.5	179	209	221	221.5	261.5	291.5	309.5	337	348	348	348	348	348	349.5	349.5	363	363	379.5	379.5	382	391	427	
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ALIGNMENTS	AAG40371	AAG14161	AAG41829	AAG41830	AAG41831	AAG40369	AAG14159	AAG40370	AAG14160	41	AAY79676	AAB31802	AAY79677	AAB31799	AAR97986	AAB31800	AAB31801	AAR97984	AAB31804	AAY95230	AAY68738	AAY68737	AAY90355	AAY25116	AAY34132	AAB18813	AAB18807	AAY87291	AAY79674	AAY79673	AAW23397	AAB31805	9035	AAY94875	
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	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia				thal	Human potassium ch	rhabd	Amino acid sequenc	rhabd	Amino acid sequenc		Amino acid sequenc	Amino acid sequenc	DmORF1 potassium c	Amino acid sequenc	Mouse potassium ch	KT5, a TWIK family		Human TWIK-4 prote	Human hTREK-1 prot	Human potassium ch	Protein encoded by	acid se	signal pe	יסי	Human potassium ch	\vdash	Amino acid sequenc	TWIK-3 E	Human protein clon	

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RESULT
AAY34133
19-JAN-1999;
25-FEB-1998;
07-AUG-1998;
                    WPI; 1999-527591/44.
N-PSDB; AAZ11915.
                                                                                                                     02-SEP-1999.
                                                                                                                                                                Potassium channel; ataxia; arrhythmia; epilous Bartter's syndrome; cardiovascular disorder; CNS disorder; renat disorder.
                                                                                                                                                                                       Human potassium channel K+Hnov59
                                                                                                      22-FEB-1999;
                                                                                                                                   WO9943696-A1
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                      30-NOV-1999
                                                                                                                                                                                                                     AAY34133;
                                                                                                                                                                                                                                   AAY34133 standard; Protein;
                                                        (AXYS-) AXYS PHARM INC.
                                          MΕ,
                                          Hu P,
                                                                                                                                                                                                     (first entry)
                                                                       99US-0116448.
98US-0076687.
98US-0095836.
                                                                                                      99WO-US03826
                                           Miller
                                           AP,
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                                           Rutter
                                          ĭ
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New nucleic acids encoding mammalian K+Hnov por issium channel proteins, useful for the diagnosis and treatment of episodic

ataxia

cardiac arrhythmia, epilepsy and Bartter's syndrome

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RESULT
AAY28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is a 4 transmembrane domain, 2 pore domain potassium channel. The gene is located on chromosome 19, determined via PCR chromosomal localisation using primers AAZ11939 and AAZ11940. K+Hnov cDNAs considered by extension of expressed sequence tags (EST9) which were related but not identical to known human potassium channels. Potential collegendent clones. Potassium channels have critical roles in various (cell types and biochemical pathways. Defective potassium channels are cknown to cause four human diseases: episodic ataxia with myokymia; cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome. CR As potassium channels are critical components of virtually all cells, ci is likely that abnormal potassium channels are also implicated in certain renal, cardiovascular and central nervous system (CNS) ci dentifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnov protein and in studying the CR biochemical pathways associated with it. They may also be used for the cepublicant production of k-Hnov protein in fermentation cultures. CR Additionally, such nucleotides may be used in gene therapy protocols for the treatment of diseases associated with abnormal potassium channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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K+Hnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov59
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                                                                                                         361
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                                                                                                AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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                                                                                                                                                                                                            KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ
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Pred. No. 1.9e-209;
1; Mismatches 0;
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DXXXI

AAY28496 standard;

Protein; 411

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12-OCT-1999 AAY28496;

(first entry)

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                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 410
                                                                                                                                                                                                                                                                                                                                           This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1 polypucleotide AAZ00039. h-TREK1 is a two pore potassium channel, and the gene maps to human chromosome 1q32, between the markers D1S237 and WI5105. The polypucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diamnosis may be used in the treatment of diseases including cancer, pulmw.nary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulmonary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chapman CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1998;
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                   stroke, and head trauma and neurological dis. ders including migraine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999
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ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
                   kktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsikrklsaelagnhnq
                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Page 24; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pore potassium channel used for, e.g. treatment of cancer,
ry, cardiovascular and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; two pore one lone 1q32.
                                                                                                                                                                                                                                                                                                                 411 AA;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meadows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potassium channel; inflamm.
                                                                                                                                                                                                                                                                         99.8%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  2P domain potassium channel family of proteins which play a part in the control of resting membrane potential. Modulation of these channels will therefore affect neuronal excitability, thereby leading to a modulation of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain neurological conditions such as anilance.
                                                                                                                                                                                                                                                neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy, incontinence, erectile dysfunction or alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TREK; 2P domain potassium channel; resting membrane potential; neuronal excitability; neurotransmitter release modulation; epilepsy; neurological disorder; sleep-related disorder; cognitive dysfunction; attention deficit disorder; addiction; anxiety; phobia; Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of human TREK1 polypeptide, polynucleotides encoding them and modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related disorders, addiction and dyskinesias including Parkinson's and Huntington's chorea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000; 2000WO-GB02107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erectile dysfunction; alopecia.
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2001-080422/09
                                                     gatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaainagiiplgnt
                                                                   GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT
                                                                                                          maapdlldpksaaqnskprlsfstkptvlasrvesdttinvmkwktvstiflvvvlylii
                                                                                                                                                                 410;
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Pred. No. 1
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1.9e-209;
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1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVHKKTVSTIFLVVVLYLII

Matches Query Match Best Local

Similarity

96.9**%;** 95.9**%**;

Score 2035; DE 2... Pred. No. 3.4e-203;

Length 411; Indels

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Gaps 60

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Conservative

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RESULT
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              This sequence is the mouse h-TREK1 polypept! . encoded by the h-TREK1 polypucleotide AAZ00040. h-TREK1 is a two per potrassium channel. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diaments may be used in the treatment of diseases including cancer, puln cary, cardiovascular, and inflammatory diseases including cancer, polipers including depression and schizophrenia, neurodegenerative diseases including Alzheimer's, stroke, and head trauma and neurological dispreces including migraine.
                                                                                                                                                                                                                                                                                                                                                                           h-TREK1; two pore potassium channel; inflamma .ry disease; chromosome 1q32.
                                                                                                                                                                                                                  Chapman
                                                                                                                                                                                                                                                           09-OCT-1998;
27-JAN-1998;
Sequence
                                                                                                                                                             New two
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                                                                                                                                                                                                                                                                                                                                                        Mus musculus.
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                                                                                                                                                  pore potassium channel used for, e.
ry, cardiovascular and inflammatory
                                                                                                                                                                                  AAZ00040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                           Page 26; 44pp; English.
411
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98EP-0300570.
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RESULT
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                               The present sequence represents a mechanically sensitive potassium channel protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with
                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                            New mechanically sensitive potassium channel, use specific modulators, potential therapeutic agents system disorders
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disease; epilepsy; cardiovascular disease; arrhythmia;
on; ischemia; anoxia; hormone secretion abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
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Best Local
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     WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues also as therapeutic inhibitors or activators.
                           Chapman
                                                         03-NOV-1998;
07-OCT-1999;
                                                                                                                                        Human; h-TRAAK; potassium channel polypeptid
2P domain potassium channel; neurodegenerati:
psychiatric disorder; neurological disorder; "
                                                                               03-NOV-1999;
                                                                                                            WO200026253-A1
                                                                                                                                                                     Human h-TRAAK polypeptide
                                                                                                                                                                                                    AAY94425;
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                                                                                                                                                                                                                   AAY94425 standard;
                                          (SMIK )
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                            Duckworth
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99GB-0023668
                                                                               99WO-GB03634
                                           BEECHAM
                                                                                                                                                                                                                   Protein;
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96.7%;
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Pred. No. 3e-1877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                              03-NOV-1998;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                 Human; h-TRAAK; potassium channel polypeptide;
2P domain potassium channel; neurodegenerative disease; stroke;
psychiatric disorder; neurological disorder; Gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY94426 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       schizophrenia, neurodegenerative disease including Alzheimer's, stroke and head trauma and neurological disorders including migraine and epilepsy. The present sequence is human h-TRAAK protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polypucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                     03-NOV-1999;
                                                                                                                                                                                                             11-MAY-2000
                                                                                                                                                                                                                                                                     WO200026253-A1
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human h-TRAAK polypeptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated h-TRAAK polypeptides belonging to the potassium family of polypeptides, useful for the diagnosis and treatment h-TRAAK related disorders, e.g. depression and schizophrenia -
(SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                           98GB-0024048.
99GB-0023668.
                                                                                                                                                     99WO-GB03634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BEECHAM PLC
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Pred. No. 5.
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5.2e-75;
nes 76;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Functional genomics was used to identify h-TFA: K polypeptides and h-TRAAK polynucleotides from human tissue same us. h-TRAAK polypeptides have homology to the 2P domain go ussium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK polypeptides. The h-TRAAK polypeptides and ant.qonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and schizophrenia, neurodegenerative disease in golding Alzheimer's, stroke and head trauma and neurological disorders including migraine and epilepsy. The present sequence is human h-Treak protein #2.
                                                                                                                                          Mechanically sensitive potassium channel protein: TRAAK; polyunsaturated fatty acid; arachidonic acid: iluzole; heart disease; nervous system disease; epilepsy; cardiovasculur disease; arrhythmia; neurodegeneration; ischemia; anoxia; hormone coretion abnormality;
                                                                                                                                                                                                                                                                A mechanically sensitive potassium channel precin TRAAK.
                                                                                                                muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated h-TRAAK polypeptides belonging family of polypeptides, useful for the diagn. h-TRAAK related disorders, e.g. depression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chapman
                                                                                                                                                                                                                                                                                                                         18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                    AAY30647;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY30647 standard; Protein;
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51.1%; Pred. No. 5.2e-5;
tive 61; Mismatches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a mechanically sensitive potassium channel protein designated TRAAK. The protein is activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mechanically sensitive potassium channel, used to 
specific modulators, potential therapeutic agents for 
system disorders -
                                            partial h-TREK1; two
                                                                        Partial h-TREK1
                                                                                                   12-OCT-1999
                                                                                                                                                          AAY28498 standard; Protein; 107
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                                                                                                                                                                                     9
                                                                                                                                                                                                                                        LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
                                                                                                                                                                                                                                                                                lfglayfasvlttignwlravsrrtraemggltaqaaswtgtvta
                                                                                                                                                                                                                                                                                                              CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI 278
                                                                                                                                                                                                                                                                                                                                          cifyalvgiplfgmllagvgdrlgsslrrgighieaiflkwhvppglvrslsavlfllig
                                                                                                                                                                                                                                                                                                                                                                  CIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG 218
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                                                                                                  (first entry)
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                                                                      polypeptide.
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49.8%;
                                            pore potassium channel;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 776.5; DB 20; Pred. No. 3e-72;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                potassium channel, and the gene maps to huma; incomosome 1q32, between the markers D1S237 and W15105. The polynucle; de sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, paid, psychiatric disorders including depression and schizophrenia, neurod generative diseases including Alzheimer's, stroke, and head trauma and neurological
Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; dementia Tandem of p domains in a Weak Inward rectifying K+ channel; epilepsy; Alzhelmer's disease; Parkinson's disease; multiple sclerosis; depression amyotrophic lateral sclerosis; progressive supranuclear palsy; mania; Creutzfeldt-Jacob disease; psychiatric disorder; schizophrenic disorder; Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is a partial h-TREK1 polypepti sencoded by the h-TREK1 polypucleotide AAZ00041. AAZ00039 and AAZ284 are complete h-TREK1 polypucleotide and polypeptide sequences. h-K-K-K is a two pore potassium channel, and the gene maps to huma for comosome 1q32, between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New two pore potassium channel used for, e.g pulmonary, cardiovascular and inflammatory d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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27-JAN-1998;
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                                                                                          Human TWIK-2 protein.
                                                                                                                     04-DEC-2000
                                                                                                                                                                        AAY90356 standard;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders
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                                                                                                                                                                                                                                                                                                                                                105;
                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      including migraine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 25; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                    (first entry)
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98EP-0300570.
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                                                                                                                                                                          Protein;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                     Length 107;
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                                          depression;
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                  dementia;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              memory loss), neurological disorders (e.g. migraine), obesity, and cardiac disorders. The nucleic acids, proteins, protein homologues and antibodies against them may be further used in screening assays, predictive medicine. The nucleic acids can be inserted into vectors and predictive medicine. The nucleic acids can be inserted into vectors and used as gene therapy vectors, to express TWIK protein, to detect TWIK mRNA, modulate TWIK activity, and screen for drugs or compounds that modulate TWIK activity. Host cells may be used to produce non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease), psychiatric disorders (e.g. depression, schizophrenic disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic disorders), learning or memory disorders (e.g. amnesia or age-related memory loss), neurological disorders (e.g. migraine), obesity, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dementia, Parkinson's gisease, muitage palsy, epilepsy, Creutzfeigt sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeigt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and therapeutic agents for potassium channel associated disorders, e.g. central nervous system disorders (e.g. Alzheimer's disease, dementia, Parkinson's disease, multiple sclerosis, amyotrophic lat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWIK-2 (Tandem of P domains in a Weak Inward rectifying potassium (K+) channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as targets for developing modulating agents to regulate a variety of cellular processes. They may be useful for developing novel diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric disorders
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N-PSDB; AAA37770, AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             learning disorder; memory disorder; age-related memory loss;
neurological disorder; cardiac disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                  127
                                                                                                                                                                                                                                       114 IIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
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                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                               54 VVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAG
                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSA
                                                                                                                         ltwi-salgkffggrakrlgqfltkrgvslrkaqitctvifivwgvlvhlvippfvfmvt
                                                                                                                                                                      LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHI 233
                                                                                                                                                                                                                                                                                                      iifylaigaaifevleephwkeakknyytqklhllkefpclgqegldkilevvsdaagqg
                                        egwnyieglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
                                                                                     EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI 292
                                                                                                                                                                                                               vaitgnqt--fnnwnwpnamifaatvittigygnvapktpagrlfcvfyglfgvpl---c
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31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 427; DB 21;
Pred. No. 9.9e-36;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 499;
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RESULT 1
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                                     TASK1 (see AAY79674). TASK2 is a unique pot ssium transport channel that is regulated by external pH, and is pro luminantly expressed in kidney and epithelial tissues. The invention relates to: identification of the native renal channel with the properties of TASK2; identification of potent pharmacology that specifically modulates the activity of the TASK-2 channel; localizing K+ channels comprising the TASK2 subunit in vives and the generation
                                                                                                                     The present sequence is that of human TASK2 (TWIK-related acid-sensitive potassium channel 2), a novel member of the 2P domain potassium channel family that also includes !WIK-1 (see AAY79673) and
                                                                                                                                                                                      New nucleic acid encoding a non-inactivation outwardly rectifying potassium transport channel, designated TASK, useful in the treatof hypertension or dysfunctions of the kidne, liver or pancreas
                              of mice in which the TASK2 gene has been in privated.
                                                                                                                                                                                                                                                      WPI; 2000-376487/32
                                                                                                                                                                                                                                                                            Duprat F,
                                                                                                                                                                                                                                                                                                                                                           09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                         08-NOV-1999;
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                                                                                                                                                                      Fig 14a; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channel; drug
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99US-0436265
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diagnostic tests and therap () ic methods
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77
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113..133
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                             generation The invention
                  to: detect
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24-JUL-1998;
07-AUG-1998;
25-AUG-1998;
09-SEP-1998;
29-SEP-1998;
                                                                                                                                                                                                                                                                                                            cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; osteoporosis; osteoparthritis; periodontal disease; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury
                                                                                                                                                                                                                                                             systemic cytokine damage; tissue differentiation; contraceptive; coagulation disorder; myocardial infarction; inflammatory conditiseptic shock; sepsis; ischaemia; reperfusion injury; arthritis; t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and treat human pancreas and/or
                                                                                                        22-JUL-1999;
                                                                                                                                          03-FEB-2000
                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY94875 standard; Protein; 499 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modulating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 e-ssphs----rkalqvkgstaskdvnifsflskkeety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 VVLYLIIGATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIQQIVAAINAG 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   creas and/or liver dysfunctions that may arise from mutatt TASK2 gene; protect against tissue rejection in kidney, liver transplants; and identify potential drugs capable ulating TASK2 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELAGNHNQELTPCRRTLSVNHLTNERDV--LPPLLKTESIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 egwnyieglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHI 233
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                                                                                                                                                                                                                                                                                                                                                                                                  protein; hydrophobic domain; nutritional source; haematc
ine production; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                             therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone HP10538
                   98JP-0208820.
98JP-0224105.
98JP-0238116.
98JP-0254736.
                                                                                                        99WO-JP03929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.3%;
31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
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Pred. No. 9.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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of
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conditions such as asthma, and in immune suppression after organ
conditions such as asthma, and in immune suppression after organ
conditions such as asthma, and in immune suppression of haematopoiesis
cand consequently in the treatment of myloid cell
conditions. It is also used in composition or lymphoid cell
conditions it is also used in composition or lymphoid cell
conditions. The protein is also used in the treatment of osteoporosis
conditions of it is also used in the treatment of protection is used
conditions of disease. The protein is used
conditions of disease. They are useful for protection or regeneration and
conditions of disease. They are useful for protection or regeneration and
conditions and conditions resulting from system contraction. They are
also used for promoting or inhibiting tissue. Efferentiation. They are
also used as contraceptives since they exhibition or inhibit related
activities and as a fertility inducing there is contracted to the conditions resulting from coagulation activities e.g. myocardial
conditions resulting from coagulation activities e.g. myocardial
conditions or agonists of receptor/ligand in practions. They are used to
inhibitors or agonists of receptor/ligand in practions. They are used to
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 106; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other cytokines in certain cell populations. We protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potential genetic disorders. The DNA and pro in can also be used as nutritional sources or supplements. The prot exhibits cytokine, cell proliferation, cell differentiation activities and induces production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human proteins having hydrophobic doma iseful costeoporosis, Alzheimer's disease, Parkinson Vaisease, multiple sclerosis, rheumatoid arthritis, calife, anaem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAGA )
(PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 245-247; 351pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infectious diseases caused by viral, bacterial, fungal or other infections. The protein is also used for treating autoimmune di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic marker. The protein can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                 prevent tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treat inflammatory conditions such
                                     186
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                                                                                                         127
                                                                                                                                                                              72
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                                                                                                                                                                                                                                                                                      54 VVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQH.
              iifylaigaaifevleephwkeakknyytqklhllkei; gqegldkilevvsdaagqg
 GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRF
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31.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a human protein of
                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                        ے 427;
م
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(es (.2);
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TYDKFQRATSIKRKLSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention, which
                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                           Indels
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ker, and to
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RESULT
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                                                   e.g. central nervous system disorders (e.g. Alzheimer's disease), dementia, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jacob disease), psychiatric disorders (e.g. depression, schizophrenic disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic disorders), learning or memory disorders (e.g. amnesia or age-related memory loss), neurological disorders (e.g. migraine), obesity, and cardiac disorders. The nucleic acids, proteins, protein homologues and antibodies against them may be further used in screening assays, predictive medicine. The nucleic acids can be inserted into vectors and used as gene therapy vectors, to express TWIK protein, to detect TWIK mRNA, medulate TWIK activity, and screen for drugs or compounds that modulate TWIK activity. Host cells may be used to produce non-human
                                                                                                                                                                                                                                                                                                                    This sequence represents the human TWIK-3 protein of the invention. The TWIK-2 (Tandem of P domains in a Weak Inward rectifying potassium (K+) channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as targets for developing modulating agents to regulate a variety of cellular processes. They may be useful for developing novel diagnostic and therapeutic agents for potassium channel associated disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; dementia; Trandem of p domains in a Weak Inward rectifying K+ channel; epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis; depression; amyotrophic lateral sclerosis; progressive supranuclear palsy; mania; creutzfeldt-Jacob disease; psychiatric disorder; schizophrenic disorder; Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia; learning disorder; memory disorder; age-related memory loss; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 3; 148pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1999;
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Best Local Similarity
                N-PSDB;
                                                                                                                                                                             Domain
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                                                                                                                                                                                                                                                                                   Key
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                          WPI; 2001-159864/16
                                                                                                            27-JUL-2000; 2000WO-US20439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ykngasllsntts-mgrwelvgsfffsvstittigygn, pntmaarlfciffalvgipl 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 lllaylaylalgtgvfwtlegraaqdssrsfqrdkwell; ficldrpaldslirdvvqa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ppllfshmegwsytegfyfafitlstvgfgdyvigmnpsqryplwyknmvslwilfgmaw
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                  AAF25381
                                             Gendreau SB,
                                                                                                                                                                                                                                                                                                                                                  sequence of a cpb-TWIK1 polypep:
                                                                                                                                                                                                                                                                                                                     domain weak inward potassium pr
5; TWIK6; TWIK7; TWIK1; pesticid
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274..29
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                                                                                                                                                                                                                                                              /note= "transmembrane
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                             Gillett LA,
SB, Jacobus
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                                                                                                                                                                                                                          "transmembrane domain
                                                                                                                                                                    "transmembrane domain
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                                                                                                                                                                                                                                             "Pore domain"
                                                                                                                                                                                     "pore domain"
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                                                                                                                                                                                                                                                                                                                  TWIK1; pesticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 391;
Pred. No. 3.
                                            Margolis JS
DA, Tietjen
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Nauen R
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                                             Winslow JW;
Jeschke P;
                                                                                                                                                                                                                                                                                                                               TWIK2; TWIK3;
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New tandem pore domain weak inward rectifyi: notassium

ion (TWIK)

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RESULT 15
AAW23397
ID AAW233
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Best Local :
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                                                                                     08-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-1998
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                                                                                                                                                                      08-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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    (CNRS ) CNRS CENT NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potassium channel; screening;
of P domains in a Weak Inward
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rectifying K+; antibody.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a protein confrising a potassium chann with the properties of a TWIK (Tandem of p.d. mains in a Weak Inward rectlifying K+)-1 channel. This is the first represent of a new family of channels consisting of 4 transmembrane segments and two p domains, and being only weakly rectlifying. The cDNA, vectors, the cells expressing TWIK-1 type channels and the protein are used to compensate for deficiency of potassium channels in various tissues. Compounds
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RESULT 2 T43509 T43509 T43509 probable potassium channel chain n2P38 - Caenorhab; C;Species: Caenorhabditis elegans C;Ate: 21-Jan-2000 #sequence_revision 21-Jan-200 C;Accession: T43509 R;Wang, Z.W.; Salkoff, L. submitted to the EMBL Data Library, August 1998 A;Description: Potassium channels in C. elegans. A;Reference number: Z22450	Qy 51 PLVVVLYLIIGATVFKALEQPHEISORTTIVIQKOTFISOHSCVNSTELDELIQQIVA	RESULT 1 S65566 Inward rectifier potassium channel TWIK-1 - humar C.Species: Homo sapiens (man) C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #F C.Accession: S65566 R.Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F EMBO J. 15, 1004-1011, 1996 A;Title: TWIK-1, a ubiquitous human weakly inward A, Reference number: S65566; MUID: 96183184 A; Accession: S65566 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-336 < LES> A; Cross-references: EMBL: U33632; NID: 91086490; PIDN: A Comery Match Best Local Similarity 32.5%; Pred. No. 3.6e-23; Matches 90; Conservative 62; Mismatches '98;	30 217.5 10.4 555 2 T43357 31 217.5 10.4 691 2 S46585 32 217.5 10.4 691 2 S46585 32 217.5 10.3 475 2 T27725 34 215.5 10.3 586 2 T21683 35 211 10.0 660 2 T21551 36 205.5 9.8 769 2 T27550 38 205.5 9.8 769 2 T27550 38 205.5 9.8 769 2 T27550 38 204.5 9.7 523 2 T23373 40 202.5 9.6 539 2 T23700 41 196 9.3 681 2 T19429 42 195.5 9.3 569 2 T43531 44 195 9.3 569 2 T43531 44 195 9.3 631 2 T22369 44 195 9.3 631 2 T22369 44 195 9.3 631 2 T22369 45 191.5 9.1 600 2 T24626
tis elegans text_change 21-Jan-2000	ISORTTIVIOKOTFISOHSCVNSTELDELIQQIVA 108	aar 997 #rext_change 05-Nov-1999 F: 'azdunski, M.; Romey, G.; Barhani rd 'cotifying K(+) channel with a nove pIDN:AAB01688.1; PID:g1086491 ET2 2: Length 336; e-23; e-23; Indels 17; Gaps 9;	potassium channel potassium channel outward-rectifler hypothetical prote hypothetical prote hypothetical prote potassium channel hypothetical prote

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outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32347 R;Murray, J; Wohldmann, P; O'Neal, D submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid F34D6. A;Reference number: Z21153 A;Accession: T32347 A;Status: precliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Experimental source: strain Bristol N2; clone F34D6 C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-329 <WAND
A;Cross-references: EMBL:AF083652; PIDN:AAC32863.1
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Matches 93
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Best Local
                                                                                                                                                                                                                                                                                                                                                                            Map position:
                                                                                                                                                                                                                                                                                                                                                                                            Gene: twk-23; CESP:F34D6.3
   164
                                     211
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                   KPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEE
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DLIIFCTGWGGLLIFGGAFWESSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQ
                                                                                        RTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIS
                                                                                                                                                                                                                                        MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQ-----RTTIVIQKQTFISQHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLV---FILFGLTVISAAMNLL--VLRFLTMNTEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC-VLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---DIEYLDFY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EILEATIVKSVPHKAGY------QWKESGAFYFATTVITTIGYGHSTPMTDAGKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTEL 99
                                                                   MTDAGKVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSS
                                                                                                                                      MSNA-DYETLEATIVKSVPHKAGY------OWKFSGAFYFATTVITTIGYGHSTP 108
                                                                                                                                                                      CVNSTELDELIQQIVAAI -- NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISP 150
                                                                                                                                                                                                        MKRQNIRTLSLIVCTLTYLLVGAAVFDALETENEILQVRGLGEPRKLVQRVREKLKTKYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWGGLLIFGGAFMFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQPEYV-FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSSDLIIFCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DELIQQIVAAI--NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                           102/1; 136/1; 180/1; 207/1;
                                                                                                                                                                                                                                                                           Conservative
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33.7%;
                                                                                                                                                                                                                                                                                       15.8%; Score 331.5; 32.9%; Pred. No. 2.7
                                                                                                                                                                                                                                                                         56;
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Pred. No. 2.1e-20;
                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                           265/2;
                                                                                                                                                                                                                                                                                           .7e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253
                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                         2;
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hypothetical protein K01D12.4 - Caenorhabditis e/
C;Speciles: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-19.
C;Accession: T23182
R;Dobson, R.
A; Experimental source: C; Genetics:
                                  A; Residues: 1-383 <WIL>
A; Cross-references: EMB
                                                                  A; Status: preliminary; A; Molecule type: DNA
                                                                                                      submitted to the EMBL Data A; Reference number: Z19703 A; Accession: T23182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: ORK1, a potassium-selective leak channe: with two A;Reference number: Z17770; MUID:97075152 A;Accession: T13807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potassium channel protein - fruit fly (Drosophila :lanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-199 #text_change 17-Nov-2000
C;Accession: T13807
                                                                                                                                                                                                                                                                                                                                                                                          В
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A; Residues: 1-1001 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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A;Map position: 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIFYISYLMFGAAIYYHIEHGEEKISRAEQRKAQIAINEYLLEELGDKNTTTQDEILQR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFLVVVLYLIIGATVFKALEQPHE----ISQRTTIVIQKQTF(SQHSCVNSTELDELIQQ 105
                                                                                                                                                                                                                                                                                                                                                         FKETRRRLSVEIY
                                                                                                                                                                                                                                                                                                                                                                                          FV--IVWF--IFSLGYLVMIMTFITRGLQ--SKKLAYLE.JLSSNLKATQNRIWSGVTKD
                                                                                                                                                                                                                                                                                                                                                                                                                          FYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKK----T; FEVGEFRAHAAEWTANVTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIPVNGILFAG----LGEYFGRTFEAIYRRYKKYKMSTEHHYVPPQLGLITTVVIALIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                    EMBL: 275543;
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                                                                                        translated
                                                                                                                                                                                                                                                                                                                        310
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                                                                                                                                         Library,
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                                                                                      from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 319; DE
Pred. No. 1e-17
                                                                                                                                           June
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                                                                                        GB/EMBL/DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB/EMBL/DD
                                                                                                                                                                                      rlext_change 15-Oct-1999
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                                      ;PDB:GN00023;
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                                      CESP: K01D12.4
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A; Map position: 5 A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

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RESULT 6
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
C;Accession: T19860
R;Hembry, C.
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A; Residues: 1-334 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A; Reference number: Z19188
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                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                             107
                                                                                                                                            89
                                                                                                                                                                                                              14 LILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIERITDRLKHK-YNFSERDLHLFEA 67
                                                                                                                                                                                                                                                 50
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les 85; Conserv
                                                                   GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV---
                                                                                                  GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG
                                                                                                                                                           VAAINAGIIPLGNTSNQISH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                        IFLVVVLYLIIGATVFKALEQPHEISQRTTIV----IQKQTFISQHSCVNSTELDELIQQI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACFFYCLSNVSSIVVRQLLNWM---IKKMDVKV-EDRSFLC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAYF-----AAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TASAGIYSVVENWNYIDSLYFCFISFATIGFGDYVSNQQDVTRMSPDLYRFVNFCLLTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----IVSGTYMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIM 233
                                CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYV--AGGSDIEYLDFYKPVVWF
                                                                                                                                          IA-----IKSIPQQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL--DFYKPVVWFWILVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATVISTIGFGTSTPRTHLGRFITIVYGVVGCTCCVLFFNLFL----ERLVTGMSYILRS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTVITTIGFGNISPRTEGGKIFCIIYALLG----IPLFGFLLAGVGDQLGTIFGKGIAK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDNRMADYQKVYCKHKPLNECDFEEMVRFISDGATSGLL-----NSRSRFDHLGSLFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRANTLPSITRAKVGCFARLRIYEENARFVLICIILIVYLAFGAILFHWLEWENEVDERI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSFSTKPTVLASRVESDTTINVMKWKT-VSTIFLVVVLYLIIGATVFKALEQPHEISQRT
                                                                                                                                                                                                                                                                                                                                                                        60/2; 98/1; 145/3; 160/3; 181/1;
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: 270266; PIDN: CAA94204.1;
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                                                                                                                                                                                                                                                                                                    13.5%;
27.4%;
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                                                                                                                                                                                                                                                                                Score 284.5; DB:
Pred. No. 1.7e-15
3; Mismatches 11:
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Pred. No. le-15;
0; Mismatches 1
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A; Accession: T43394
A; Status: preliminary; translated
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C;Accession: T43361
C;Accession: T43361
Lotary, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43361
                                                                                               R;Kunkel, M.T.; Salkoff, L. submitted to the EMBL Data Library, AA;Description: Potassium channels in A;Reference number: Z22479
                                                                                                                                                                         potassium channel chain n2P18 homolog - Caenorhabditis elegans C;Specles: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_chang.C;Accession: T43394
                  A; Molecule type: mRNA
A; Residues: 1-461 < KU
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A; Residues: 1-364 <WAN>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIV---IQKQ1F1SQHSCVNSTELDELIQQI 106
                                                                                                                                                                                                                                                                                                                                     LERFTRNSLVDSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                          WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAAINAGIIPLGNTSNQISH-WDLGSSFFFAGTVITTIG; ;NISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVLFVALPATIFKHIEGWSALDATYFVVITLTTIGFGD> -- AGGSDIEYLDFYKPVVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV--
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                                                                                                                                                                                                                                                                                                                                                                          YDKFQRATSIKRKL
                                                                                                                                                                                                                                                                                                                                                                                                                FILIGLAVESACVNLL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IVSGTYMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IA-----IKSIPQQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF
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  EMBL: AF083650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AF083646;
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Pred. No. 1.
                                                          from GB/EMBL/DD3J
PIDN:AAC32861
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C. elegans
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submitted to the EMBL Data Library, March 1997
A; Reference number: 720027
A; Accession: 725392
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-393 <NIL
A; Residues: 1-393 <NIL
A; Experimental source: clone T28A8
C; Genetics:
A; Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T28A8.1 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T25392 R;Lloyd. C.
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TTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPLILITVADIGKFLSENIVQLYTWYRKL
                                                  AGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGD------QLGTIFGKG
                                                                                                               EMRESGIGQHVVEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDYNWTYMTALFF
                                                                                                                                                                     -- QHSCVNSTELDELIQQIVAAINAGIIPLGNT------
                                                                                                                                                                                                                             WKTYARIILAHVSLIVLSVVYVGFGAFLFYQLEQPNEVEVRARNIERFNIHKRQMIEHLW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILTTFQKTFKGLLPLIILVAYTLLGAWIFWMIEGENE-----REMLIEQQK---
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                                                                                                                                                                                                                                                                                                                                            Conservative
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23.5%;
                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 279; DB 2; 27.0%; Pred. No. 5.7e-15;
                                                                                                                                                                                                                                                                                                                                            54;
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                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                            107;
                                                                                                                                                                                                                                                                                                                                                                                            Length 393;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                  SNQISHWDLGSSFFF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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hypothetical protein C24A3.6 - Caenorhabditis C;Species: Caenorhabditis elegans C;sate: 20-Sep-1999 #sequence_revision 20-Sep-C;Accession: T15584 R;Favello, T.
                                                                                                                RESULT
T15584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, I tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A;Reference number: $43531; MUID:94150718
A;Accession: T45032
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 ** ** cext_change 21-Jul-2000 C;Accession: T45032
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A; Introns: 47/2;
A; Note: Y39B6B.f
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A; Residues: 1-392 <WIL>
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submitted to the EMBL
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les 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                        EGWSALDAIYEVVITLTTIGFGDYVAGGSDIEYLDFYKPVVNFWILVGLAYFAAVLSMIG 293
                                                                                                                                                                                                                              YKPVVWFWILVGLAYFAAVLSMIGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDPKSAAQNS----KPRLSFSTKPTVLAS----RVESDTTINVMKWKTVSTIFLVVVLY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAKVEDTFIKWNVSQTK-----
                                                                                                                                                                                          YKIGATVYLMGGLCCMMLFLATLYD
                                                                                                                                                                                                                                                                                                                                                PLTLALLSAIVARMREPSHKLRGLLNQRLGHLF - - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -FSRIEYPLE-----KIEREAYLDYQNQWRDRLIQLDIDESEIDKLFLNIRE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82/2;
Data Library,
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                                                                                                                                                                                                                                                                                                                                                                                    --GDQLGTIFGKGIAKVENTFIKWNVSQTKIRIISTI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 273; DB 2;
Pred. No. 1.7e-14;
6; Mismatches 10C
November
                                                                                                                                                                                                                              294
                                                        20-Sep-1999 *:ext_change
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                                                                                            elegans
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                                                                                                                                                                                                                                                                                          SEGDYVAGGS-DIEYLDF 269
                                                                                                                                                                                                                                                                      GLGDFEPGDDPNQSFRGL
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                                                                                                                                                                                                                                                                                                                                                ----TVNHIQLIHVG
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                                                          20-Sep-1999
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T24265
R;Wilkinson, J
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T24265
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A; Residues: 1-522 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, March 1996 A; Reference number: Z19866
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A; Introns: 21/1; 63/3; 131/1; 193/3; 206/3
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C;Genetics:
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A; Residues: 1-325 <FAV>
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A;Accession: T15584
                                                                                                                                                                                                                                                                                                              A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T01B4.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                       A; Introns:
                                                                                                                                                                                                                                                        Map position: X
                                                                                                                                                                                                                                                                         Gene: CESP:T01B4.1
                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:270036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4; Experimental source: clone T01B4
                                                                                                                                                              Query Match
Best Local Similarity
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                                                                    LILIILGYACLGGYMFQALEYDQQQLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQSNE 100
                                                                                                       IFLVVVLYLIIGATVFKALEQPHE-----ISQRTTIVIQKQTFISQHSCVNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PIVGVLLLIGLSLVSTVMTLIQQQIEALASVRRKKKKK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS----KKTKE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TIIFILFGCVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKGIAKVEDTFIKWNVSQTKIRIIS------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STELDELIQQIVAAIN------AGIIPLGNTSNQIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVSTIF-----LVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVN
                 LDELIQQIVAAINAGIIPLGNTS-NQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSFPISGLLLITVIWVIFCAVLETFLEEWDFGTSLYFTLISFTTIGFGDILP--SDYDFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ERDELIRRTVYKINQLQIKRQRRLMTAEEEYNRTAKVLTTFQETLGIVPA--DMDKDI 112
----KRCLELITKTFIQRSDEERGEGWRWDFWNSVFFSATIFTTIGYGNLACKTNLGRI 155
                                                                                                                                                                                                                                   95/3; 142/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66;
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                                                                                                                                                                                                                                   224/3; 290/1; 458/3
                                                                                                                                                              12.7%;
23.1%;
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; Pred. No. 2.9e-14;
53; Mismatches 88
                                                                                                                                           64;
                                                                                                                                         Score 266; DB 2; 1
Pred. No. 9e-14;
4; Mismatches 132;
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                                                                                                                                                                              DB 2; Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length, 325
                                                                                                                                           Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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submitted to the EMBL Data Library, A; Reference number: Z19377 A; Accession: T21118
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A;Molecule type: DNA
A;Residues: 1-452 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Swinburne, J.; Ainscough,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:F19D8.1
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Best Local
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276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 LKISGGRRSSSDASSVITEASDEDTRHFKVGRAILAEA: DERASNHGTQLNSCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 MLEVFFEVPEDDKEDTTFQLRWG-------LLV:VLFVVLCSFVVSFWENWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189
                                      256 DYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDELEVI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 FLTAFYFFEVSLSTIGFGDIVP------DHPRTACALEVLYFIGLALFAMVYAILQER 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 ATTIYGMIGIPLMLFYLKNFGELCYKWAKKIQFNYQQCLKK::FGRKQKRASSLASITSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 FCIIYALLGIPLFGFLLAGVGD------
                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                                                 42 MKWKTVSTI------FLVVVLYLIIGATVFKALE--- PHIBISQRTTIVIQKQTFIS
                                                                                                                                                                                                                                96 LATTENVAEINEHLRMFLRNISNLHISLDNYLIFNEPTQIVIKRWTFPSSVLFSFTILTT 155
                                                                                                                                                                                                                                                                      90 QHSCVNSTELDELIQQIVAAINAGIIPLGN-----TSNO\SHWDLGSSFFFAGTVITT 142
                                                                            EHLLREIAEVSPYLDVLLVAGLFVVFIAIGSAVIPLWENQLTYFDSVYFSYMSLTTIGLG
                                                                                                              QTKIRIISTI----IFILFGCVLFVALPAIIFKHIEGW----SALDAIYFVVITLTTIGFG
                                                                                                                                                    IGYGNVTPHTQQCKVFLMIYGAFGIPLFLITIADLGRFSKTALMALVQKVSKRELKKQSD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWII. - - VGLAYFAAVLSMIGD-
  DIVP-----RRMDFLLPTL-IYITIGLWLTTALVEQLADVEKLV 313
                                                                                                                                                                                          IGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTLFGKGIAKVEDTFIKWNVS
                                                                                                                                                                                                                                                                                                             MKFRNVLRIALGHLALYCFVVCYVFAGAWVFHQLEGENI.FI IDKQREYAMNLKKDVIAK 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----W-LRVISKKTKEEVGEFRAHAAEWTANVT----
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         12.5%;
                                                                                                                                                                                                                                                                                                                                                                                         50;
                                                                                                                                                                                                                                                                                                                                                                                       Score 262; DB
Pred. No. 1.6e
50; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 452
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                              275
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RESULT

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: EMBL:Z82073; PIDN:CAB04923.1; GSPDB:GN00023; CESP:W06D12.2
A;Experimental source: clone W06D12
A;Experimental source: clone W06D12
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R;Thomas, K.
                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein W06D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26229
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A;Accession: T27881
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-427 <MILD
A;Residues: 1-427 <MILD
                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, November 1996
A;Reference number: Z20177
A;Accession: T26229
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T26229
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A;Map position: 2
A;Introns: 51/3; 123/1; 212/1; 261/2; 331/3; 365/1; 394/2; 414/3
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                                                                                                              A; Map position: 5
A; Introns: 70/3; 127/1;
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A;Experimental source: clone ZK1067
  Matches
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                         Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
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                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YMTISACVYTILEPMWSFLDSFYFCLVSLLTVGFGDLHPVGT-VEYM-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LCSIVFIFIGLILTTLAVDVSGSVGIAKMHSIGRGFDAMKMLNALRKKETVK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLFVALPAIIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VA----AINAGIIPLG-NTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCII 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAIFGIPL---TLVTIAD-----LAKFVADMLIMDPTEDPKTGRQLLVLVFLLG--
    81;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 249.5; DB ilarity 26.3%; Pred. No. 1.5e-1 Conservative 59; Mismatches 1
                                                                                                              170/1; 197/3; 326/1; 405/3
11.8%; Score 247; DB 2; I
20.8%; Pred. No. 2.5e-12;
live 75; Mismatches 125;
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                                           Length 444;
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  Indels 108;
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  Gaps
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    11;
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Search completed: August 28, 2001, 17:07:04 Job time: 473 sec

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مراجع والمتحارث أأواه

	354	334	299	292	251	237	198	208	138	155	83	95	23	53	
get Pa T.	354 GNVAEKYSENMEMGNKLLMRFMSNHQKKM 382	VEIYDKFQRATSIKRKLSAELAGNHNQEL 362	IQMQLEFIFNQIVQRIENDFKNTLSVAAEESRKK3.VSEFGSIDPSKKKTMRTD 353	IGDWLRVISKKTKEEV-GEFRAHAAEWTANVTAEFKETRRRLS 333	TLFESVYFFFISMTTIGFGDFTPSHTVAVGGIVFILGGLSVVSMCINV 298	237 SALDAIYEVVITLTTIGEGDYVAGGSDIEYLDEYKPVVWEWILVGLAYFAAVLSM 291	GSIDKTPLMETSSTPPSPQNPNGTRPIPLLLVLIVLFFWMIQCVAYFAYFENW 250	IISTIIFILFG:VLFVALPAIIFKHIEGW 236	GRICTMIXAMIGIPIVINILNDWGNMLFYFVDHFWQNIGRQW!OSLRQKLRRKVQSLEE 197	GKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIR 207	S SETKLRRYLSEYDAAMGISIDSKMKTRWDINGGLYYAGTIYTTIGYGDLAAETIW 137	NSTELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSF FACTVITTIGFGNISPRTEG 154	23 VLIVYSFLGAGLFVLCEAENEKSLKHEDNMRVLRTSIAA "VFVQRLQNMYSGNGSSSEF 82	VVVLYLIIGATVFKALEQPHEISQRTTIVIQK)FFISOHSCV 94	

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425026 segs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAAPDLLDPKSAAQNSKPRL.....LNGLTPHCAGEEIAVIENIK 411
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Copyright (c) 1993 - 2000 Compagen Ltd.
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                 Ognrt2 homo sapien
Ogjis4 rattus norv
Oghb59 homo sapien
Ogj591 homo sapien
Ogj582 mus musculu
Ogz12 rattus norv
Ogj158 cavia porce
Ogg158 rattus norv
Oghb68 homo sapien
Ogf195 caenorhabdi
Ogeru5 rattus norv
Ogh592 homo sapien
Ogg34 mus musculu
Ol7188 caenorhabdi
Ol7188 caenorhabdi
                                                                                                                                                                                                 Description
 Q9hb15 homo sapien
           Q9es08 rattus norv
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	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20			
	236.5	240	243	243.5	244.5	245.5	247	249.5	261.5	262	266	269	273	273	279	280	282.5	284.5	284.5	287.5	288	293.5	296.5	299.5	300	301		,	777
	11.3	11.4	11.6															13.5						14.3		14.3			
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- 7.	•																					٠.			Т.	(1)	K.	<u>خ</u> ر'	
	P90863 caenorhabdi		a.	Q9j157 cavia porce				Q23386 caenorhabdi		Q93531 caenorhabdi		Q18120 caenorhabdi			Q9xu07 caenorhabdi	$^{\circ}$	09tzp8 caenorhabdi		_	Q9hb14 homo sapien	Q21094 caenorhabdi	Q9esm5 rattus norv	09vfs9 drosophila	Q9jjl4 mus musculu	09vhe0 drosophila	Q9ers1 rattus norv		,	100

ALIGNMENTS

Qy 121 SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC : 11LGIPLFGFLLAGVGDQ

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RESULT

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Best Local
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Interpro; IPR000099; -..
Interpro; IPR001622; -..
Interpro; IPR003280; -..
Interpro; IPR003280; -..
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01333; 2POREKCHANEL.
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Q9JIS4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 275:17412-17419(2000).
EMBL; AF196965; AAF75132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20298807; PubMed=10747911;
Bang H., Kim Y., Kim D.;
"TREK-2, a new member of the mechanosensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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 296
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63.7%;
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Last annotation update)
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Pred. No. 6.2e-82
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RESULT
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Q9H591;
Q9H591;
01-MAR-2001
01-MAR-2001
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Query Match
Best Local Similarity
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J. Biol. Chem. 275:28398-28405(2000).
EMBL; AF279890; AAG15191.1;
IONIC Channel.
SEQUENCE 538 AA; 59764 MW; 8EA615B08D147;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
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Eukaryota; Metazoa; Chordata; Craniata; Vertel sta; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homo idae; Homo.
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                         350 LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
                                                    NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170
                                                                                                                                                                                                                                                                                                                                                                  AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASF\\ SDT---TINVMKWKTVSTI
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                                                                                                                                                                                                                                                                                                       FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISCHSCVNSTELDELIQQIVAAI 110
 -SME--
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                                                                                                                                                                                                                                                                                           FVVVVVLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD
                                                                                                                                                                                                                                                                                                                                                 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RF; 3:1SQGGLQTVMKWKTVVAI 75
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                                                                                                                                                                                                                                                                                                                                                                                                                     59.2%;
62.7%;
RRRLGLDQRAHSLDMLSP
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Pred. No. 1.
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394
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(TrEMBLrel. (TrEMBLrel.

16, 16,

Created)
Last sequence update)

PRELIMINARY;

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RESULT
Q9JK62
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OJK62;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
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DJ137F1.2 (N
                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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                                                                                                                                                                                                                                                                                                     Roux J., Barhanin J.; "Mouse two P domain p
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=129/SVJ; TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Mammalia; Eutheria;
    SEQUENCE
                                          PRINTS; PR01333; 2POREKCHANEL
                                                               InterPro; IPR001622; -.
InterPro; IPR003280; -.
                                                                                                                                                                                                                    TISSUE=KIDNEY;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLG 166
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  ΑĄ.
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Rodentia;
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Primates;
                                                                                                                                                                                                                                                                                 potassium channel TASK2.";
) to the EMBL/GenBank/DDBJ
55976 MW;
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OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 502.5; DB 4
Pred. No. 1.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
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E4C7E7CC71B44D95 CRC64;
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Matches
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                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                     O9ZZT2 PRELIMINARY; PRT; 336 AA O9ZZT2; O1-MAY-1999 (TrEMBLrel. 10, Created) O1-MAY-1999 (TrEMBLrel. 10, Last sequence of the other control of the potastive potastium Channel TWIK.

PUTATIVE POTASSIUM CHANNEL TWIK.

PARTLUS NOTVEGILOUS (Bat).
                                                                                                                                                          InterPro; IPR003280; -.
Pfam; PP02034; TWIK_channel; 1
PRINTS; PR01036; TWIK1CHANNEL.
PRINTS; PR01096; TWIK1CHANNEL.
                                                                                                                                                                                                                                     "Cloning and localization of TTWIK, a putative votassiuntwo P domains.";
Submitted (SEP-1997) to the EMBL/GenBank/DDB1 3-tabases
EMBL, AF022819; AAD09336.1;
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertel Jta; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Midae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                        Ionic channel SEQUENCE 3
                                                                                                                                                                                                                                                                                 Gan L., Joiner
Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                             InterPro;
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          AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGRUS REGGK1FCIIVALLGIP 168
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                                                                                              Similarity
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                                                                                                                                                                                                                             IPR000099; -.
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                                                                                   Conservative
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                                                                                                                                        38228 MW;
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32.5%;
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                                                                                           Score
Pred.
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Pred. No. 7.
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                                                                                  Gaps
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InterPro; IPR000099; ...
InterPro; IPR001622; ...
InterPro; IPR003092; ...
InterPro; IPR003280; ...
InterPro; IPR003280; ...
Pfam; PF02034; TMIK_channel; 1.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "TASK-3, a novel tandem proe domain acid-sensitive extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16550-16557(2000).
EMBL: AF212827; AAF63706.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-OCT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
POTASSIUM CHANNEL TASK3.
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MEDLINE=20287530; PubMed=10747866;
MEDLINE=20287530; PubMed=10747866;
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Karschin A., Derst C.;
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                                                 NVTAEFKETRRR 331
                                                                                                   RKPFYVAFSFMYILVGLTVIGAFLNLV--VLRFLTMNSDEERGEGEEGAALPGNPSSVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.0%; Score 357.5; DB 11; 30.1%; Pred. No. 4.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40769 MW;
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Q9NPC2; Q9NPC2; Q9NPC2; Q9NPC2; Q9NPC2; T 01-CCT-2000 (TrEMBLrel. 15, Last sequence of the control of the contr
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O02821;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence u. 'ure)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation uprate)
DOUBLE PORE POTASSIUM CHANNEL RABKONKI (FRACHENI).

Oryctolagus cuniculus (Rabbit).
Cukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Cryrtolagus.
                                                                                                                                                                                                      Girard C., Lesage F., Tinel N., I "Human Task-3, a novel 2P domain Submitted (JUN-2000) to the EMBL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
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                                      SEQUENCE FROM N.A.
MEDLINE=20287530; PubMed=10747866;
Rajan S., Wischmeyer E., Liu G.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Veruebrata;
Mammalia; Eutheria; Primates; Catarrhini; Haricidae.
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InterPro; IPR003280; -.
PRINTS; PR01333; 2POREKCHANEL.
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                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTLLFLTAVVQRVTVHVTR---RPVLYFHVRWGFSKQVVA1VHAVLLGLITVSCFFFIPAA
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78; Conser
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259 AA;
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33.1%;
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Pred. No. 3.4e-18;
7; Mismatches 94
                                           G.X.,
Preisig-We;
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POTASSIUM CHANNEL).
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EMBL; AF21889; AAF65708.1; -.

EMBL; AF21889; AAF63708.1; -.

EMBL; AF21889; AAG33126.1; -.

EMBL; AF248241; AAG31730.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "TASK-3, a novel tandem proe domain acid-sensitive extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
  Q9HBC8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003092; -.
InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
                       Q9нвс8
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Vega-Saenz de
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Local Similarity 27.0%;
mes 106; Conservative 7
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                                                                                                                                            VTAEFKETRRRLSVEI
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                                                                                                                                                                                                                                                FCMEYAVLGIPLTLVMEQSLGERM------NTEVRYLLKRIKKCCGMRNTDVSM
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                                                                                                 RTLSVNHLTNERDVLPPLLKTESIYLNGLTPH
                                                                                                                                                                 KPLYVAFSFMYILVGLTVIGAFLNLV--VLRFLTMNSEDERRDAEERASLAGNRNSMVIH
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  (TrEMBLrel.
                        PRELIMINARY;
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  Created)
                                                                                                                                                                                                                                                                                                                                                                                        Score 349.5; DB 4;
Pred. No. 1.7e-17;
7; Mismatches 146;
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                       PRT;
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C 076795;
T 01-NOV-1998 (TrEMBLrel. 08, Created)
JT 01-NOV-1998 (TrEMBLrel. 08, Last sequence up lat DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation up PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P38.
OS Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
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Vega-Saenz de Miera E
Coetzee W., Rudy B.;
"KT3.2 and KT3.3 Two
                                                                                                          Wang Z.-W., Salkoff L.; Potassium channels in C. elegans. Potassium channels in the EMBL/C Submitted (AUG-1998) to the EMBL/C EMBL; AF083652; AAC32863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to TASK1.";
Submitted (APR-2000) to the
EMBL; AF257081; AAG33127.1;
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                                      Ionic channel. SEQUENCE 329
                                                                            InterPro; IPR000099; InterPro; IPR001622; InterPro; IPR003280;
                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE 330
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Mammalia; Eutheria;
                                                         Pfam; PF02034; TWIK_channel; PRINTS; PR01333; 2POREKCHANEL
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Primates; Catarrhini; Ho
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                                       36992 MW;
16.48;
33.78;
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Pred. No. 2.1e
42; Mismatches
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EMBL/GenBank/DD
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Score
Pred.
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                                        CRC54;
          Length
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                                                                                                                                                                                         Rhabditoidea;
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RESULT
Q9H592
ID Q9
AC Q9
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ID Q99
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    Q9H592;
Q9H592;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
2P DOMAIN K+ CHANNEL TWIK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "TWIK-2, an inactivating 2P domain K+
J. Biol. Chem. 275:28772-28730(2000).
EMBL; AF:881304; AAG10508.1; -.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20435832; PubMed-10887187;
Patel A.J., Maingret F., Magnone V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ERU5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Honore E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                            195
                                                                                                                                                                                                          137
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                                                                                                                                                              233 I-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAVL
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                                                                                                                          LEEAWSFLDAFYFCEISLSTIGLGDYVPGEAPGQPYRSLYKVLVTAYLFLGLVAMVLVL
                                                                                                                                                                                                                                                                                                         LGNTSNQIS----HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EILEATIVKSVPHKAGY------QWKFSGAFYFATTVITTIGYGHSTPMTDAGKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DELIQQIVAAI--NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                       LLTASAQRLSLLLTH---APLSWLSLRWGWHPQRAARWHLVALLMVIVAIFFLIPAAVFAY
                                                                                                                                                                                                                                             LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKH 232
                                                                                                                                                                                                                                                                                     LANASGPANASDPAWDFASALFFASTLVTTMGYGYTTPLTDAGKAFSIVFALLGVPITML 136
                                                                                                                                                                                                                                                                                                                                                                YLALGALLVARLERPHEARLRAELGTLREQLLRHSPCVAAHALDAFVERVLAAGRLGRAV 76
                                                                                                                                                                                                                                                                                                                                                                                                     YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLV---FILFGLTVISAAMNLL--VLRFLTMNTEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC-VLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---DIEYLDFY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSSDLIIFCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKRQNIRTLSLIVCTLTYLLVGAAVEDALETENEILQRKLVQRVREKLKTKYNMSNA-DY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKWKTVSTIFLVV - - VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTEL
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                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34214 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               16.3%; Score 343; DB 11; Length 313; 32.2%; Pred. No. 4e-17; tive 47; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A93629568785CD8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                        229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
Q9JLD4
ID Q9JLD4
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Best Local
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R EMBL; AL136087; CACO7335.1; -.
IONIC Channel
NON_TER 229
SEQUENCE 229
                                                                   TABLE 1. PARTY II. NAME 7. THE TANDER PO TRASK-3 A NAW Member of the Tandem PO J. Biol. (Chem. 275:9340-9347(2000).

EMBL; AF192366; AAF60229.1; -.

InterPro; IPRO00099; -.

InterPro; IPRO01622; -.

InterPro; IPRO03092; -.

InterPro; IPRO03092; -.

InterPro; IPRO03092; -.

INTERPRO; IPRO03380; -.

PFAMTS; PRO10333; ZPOREXCHANNEL.

PRINTS; PRO1133; ZPOREXCHANNEL.

PRINTS; PRO1193; TASKCHANNEL.

SEQUENCE 395 AA; 44365 MW; 3F76F7!
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JLD4 PRELIMINARY;
Q9JLD4;
Q1-QCT-2000 (TrEMBLrel. 15,
Q1-QCT-2000 (TrEMBLrel. 15,
Q1-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-CEREBELLUM;
MEDLINE-20200422; pubMed-10734076;
KRIM Y., Bang H., Kim D.;
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                            POTASSIUM CHANNEL TASK3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertur ata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last Sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation 'F late)
DJ137F1.1 (NOVEL MEMBER OF THE POTASSIUM CHARAGE SUBFRAMILY K )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIPLNLVVL----NRLGHLMQQGVNHWASRLGGT---WQ-DPDKARWLAGSGALLSGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPLFGFLLAGVGDQLGTIFGKGI----AKVEDTFIKWNV OTKIRIISTIIFILFGCVL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 36.4
79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.3%; Score 342.5; P. & ... 36.4%; Pred. No. 3e-17 % tive 44; Mismatches ...
16.2%;
30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence up (te)
Last annotation (pdate)
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 Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vert orata;
Sciurognathi; Furidae;
                                                                          3F76F7923A3AFC7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7AB9FB847F242511
341; DB 11:
No. 7.5e-17;
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                                                                                                                                                                                                                                                             Channel Family.";
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Best Local Similarity 34.5
Matches 90; Conservative
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL118522; CAC14068.1; -.
SEQUENCE 330 AA; 36222 MW; 24F428721A1C7790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE
CHANNEL PROTEIN TASK (KCNK3)).
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                                                                                                                                                                                            107 VAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLG 166
233 TVIGAFLNLVVLRFLVASADW 253
                              283 AYFAAVLSMI-----GDW
                                                                                                                             118 IPLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE----NLVVAGLLACAATLAL
                                                                                                                                                               167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEV--GEFRAHAAEWTANVTAE 324
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                                                                                                                                                                                                                                                             11 LVLCTLCYLLVGAAVFDALESEAE-SGRQRLLVQKRGALRRKFGFSAEDYRELERLALQ-
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                                                            GAVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-EALQRKLPYVAFSFLYILLGL
                                                                              PAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF---WILVGL 282
                                                                                                                                                 IPLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTKIRIISTIIFILFGCVLFVAL 225
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pred. No. 7.7e-17;
2; Mismatches 96;
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Search completed: August 28, Job time: 414 sec 17:12:45

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Copyright (c) 1993 - 2000 Com
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Best I
                               19-JAN-1999;
25-FEB-1998;
07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY34133 standard; Protein;
                                                                                                                                                                                      22-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome; cardiovascular disorder; CNS disorder; renal disorder.
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Local Similarity
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                               99US-0116448.
98US-0076687.
98US-0095836.
                                                                                                                                                                                  99WO-US03826
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99.8%;
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Pred. No. 1.4e
0; Mismatches
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1.4e-217;
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This sequence represents the human K+Hnov59 po ssium channel.

CK H+Hnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, contained and may be alpha subunits, which form the functional channel, contained and may be alpha subunits, which form the functional channel, contained and may be alpha subunits, which form the functional channel, contained the form the form the functional channels and may be alpha subunits, which form the functional channels are contained by extension of expressed sequences tags (ESTs) which were contained but not identical to known human potassium channels. Potential contential polymorphisms detected as sequence variants between multiple contained to known human potassium channels are collitypes and biochemical pathways. Defective potassium channels are contained arrhythmia (long QT syndrome); epilopsy: and Bartter's syndrome. Contained arrhythmia (long QT syndrome); epilopsy: and Bartter's syndrome. Contained arrhythmia potassium channels of virtually all cells, contained that abnormal potassium channels of virtually all cells, contained the potassium channels of also implicated in certain renal, cardiovascular and central nervous system (CNS) contained the box sequences encoding them. They may be used for the contained potassium channels of the K+Hnov protein and in studying the biochemical pathways associated with it. They may also be used for the contained production of K+Hnov protein in all pene therapy protocols for the treatment of diseases associated with abnormal potassium channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids encoding mammalian K+Hnov po issium channel proteins, useful for the diagnosis and trearrest of episodic with myokymia, cardiac arrhythmia, epilepsy and Bartter's syn
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Sequence
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411
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Query Match Best Local 97.8%; 96.4%; Score 2044; DB 20; Pred. No. 3.1e-213; Length 411;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h-TREK1; two pore potassium chromosome 1q32.
                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                           stroke, and head trauma and neurological disorders including migraine.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM PLC.
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DB; AAZ00039.
                     GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
                                                                                                                                                              AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                            SNOVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                gatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaainagiiplgnt
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                                                                                                                                                                                                                                                                                                                                                                                                                                              pore potassium channel used for, e.g. trea
ry, cardiovascular and inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                              Conservative
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98EP-0300570.
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                                                                                                                                                                                                                       97.8%;
96.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          channel;
                                                                                                                                                                                                                     Score 2044; DB 20;
Pred. No. 3.1e-213;
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                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment of
                                                                                                                                                                                                                                  Length 411;
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1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAFAVEKWKTVSTIFLVVVLYLII

Matches Query Match Best Local

Local

Similarity

97.8%; 96.4%;

Score 2044; DP Pred. No. 3.1e-1; Mismatches

Length Indels

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                                The present sequence is human TREK1 (h-TREY). h-TREK1 is a member of the 2P domain potassium channel family of prote. hich play a part in the control of resting membrane potential. Modular in of these channels will therefore affect neuronal excitability, thereby leading to a modulation of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain neurological conditions such as epilepsy, significant disorders, cognitive dysfunction, attention deficit disorders, addiction, anxiety/phobia, Parkinson's and Huntington's Jurea, cerebral palsy, anxiety/phobia, Parkinson's and Huntington's Jurea, cerebral palsy,
                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal excitability; neurotransmitter releas
neurological disorder; sleep-related disorder;
attention deficit disorder; addiction; anxiety
                                                                                                                                                                                                     Use of human TREK1 polypeptide, polynucleot modulators of h-TREK1 polypeptides for treat disorders, addiction and dyskinesias included
                                                                                                                                                                 Claim 7; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erectile dysfunction; alopecia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; TREK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
Sequence
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                                                                                                                                                                                                                                                            N-PSDB;
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                         incontinence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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modulation; epilepsy;
rgnitive dysfunction;
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The present sequence represents a mechanically sensitive potassium channel protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with
                                                                                      Claim 3;
                                                                                                              New mechanically sensitive potassium channel, used specific modulators, potential therapeutic agents is system disorders.
                                                                                                                                                                                     Honore
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                                                                                                                                                                                                        (CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                    Page 23-25; 40pp; French.
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                                                                                                                                                                                                                                                                                                                                                           epilepsy; cardiovascular disease;
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Best Local S
Matches 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ischemia or anoxia), abnormalities of hormon treation and muscular disease. The protein itself may be used to the control and these diseases. Antibodies specific for the protein are use the detect it in tissues also as therapeutic inhibitors or activators.
        N-PSDB; AAA27105
                WPI; 2000-365583/31
                               Chapman CG,
                                                                03-NOV-1998;
07-OCT-1999;
                                                                                       03-NOV-1999;
                                                                                                                                                      2P domain potassium channel; neurodegenerat psychiatric disorder; neurological disorder:
                                                                                                                                                                       Human; h-TRAAK; potassium channel polypeptic;
                                                                                                                                                                                      Human h-TRAAK polypeptide
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                                                                                                                                                                                                                                         AAY94425 standard;
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                                                                                                                                        Homo sapiens
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                                Duckworth
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99GB-0023668
                                                                                       99WO-GB03634
                                                BEECHAM
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99.7%;
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Matches 145
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                                                             03-NOV-1998;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                 Human; h-TRAAK; potassium channel polypeptide;
2P domain potassium channel; neurodegenerative disease;
psychiatric disorder; neurological disorder; Gene theraj
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                                                                                                                                               03-NOV-1999;
                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                          98GB-0024048.
99GB-0023668.
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                                                                                                                                               99WO-GB03634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%; Score 797; DB 21; 51.1%; Pred. No. 7.5e-78; tive 60; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h-TRAAK polynucleotides from human tissue samp s. h-TRAAK polypeptides have homology to the 2p domain polypeptides may holypeptides. The h-TRAAK polypeptides and polypeptides may be used in diagnostic assays for conditions to led to h-TRAAK imbalance and for identifying agonists and an analysis of h-TRAAK polypeptides and polypeptides may also be useful for treatment and prevention (e.g. a vaccines) of certa diseases, such as pain, psychiatric disorders and polypeptides and polypeptides are and polypeptides and polypeptides are also be useful for treatment and prevention (e.g. a vaccines) of certa diseases, such as pain, psychiatric disorders and palabeliner's, selection of the polypeptides are also be useful for treatment and prevention (e.g. a vaccines) of certa diseases, such as pain, psychiatric disorders and palabeliner's selection of the province of the polypeptides and palabeliner's selection of the province of the polypeptides and palabeliner's p
                                                                                                   muscular
                                                                                                                                                       Mechanically sensitive potassium channel protein; TRAAK; polyunsaturated fatty acid; arachidonic acid; riluzole; heart
                                                                                                                                                                                                                            A mechanically sensitive potassium channel protein TRAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional genomics was used h-TRAAK polynucleotides from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated h-TRAAK polypeptides belonging family of polypeptides, useful for the diagnos h-TRAAK related disorders, e.g. depression and ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chapman CG,
                                                            Mus sp
                                                                                                     neurodegeneration;
muscular disease.
                                                                                                                        nervous system disease; epilepsy; cardiovascular disease;
neurodegeneration; ischemia; anoxia; hormone socretion ab
                                                                                                                                                                                                                                                                     18-NOV-1999
                                                                                                                                                                                                                                                                                                                AAY30647;
                                                                                                                                                                                                                                                                                                                                                         AAY30647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145;
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)B; AAA27106.
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                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                     (first
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51.1%;
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                                                                                                                                                                                                                                                                                                                                                         398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 797; DB 21;
Pred. No. 7.5e-78;
iO; Mismatches 77;
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RESULT
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CPT 12-C
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a mechanically sensitive potassium channel protein designated TRAAK. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues,
     Homo
                                                       chromosome 1q32
                                                                                                                                   Partial h-TREK1 polypeptide
                                                                                                                                                                                          12-OCT-1999
                                                                                                                                                                                                                                               AAY28498
                                                                                                                                                                                                                                                                                                    AAY28498 standard;
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                                                                                partial h-TREK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 49.8 es 142; Conservative
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     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as therapeutic inhibitors or activators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG
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                                                                                                                                                                                        (first entry)
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                                                                                two
                                                                                                                                                                                                                                                                                                    Protein; 107
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49.8%;
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                                                                              pore potassium channel;
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Pred. No. 5.8e-75
6; Mismatches 8
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heart a
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Best Local S
Matches 107
Human; TWIK-3; TWIK-4; TWIK-2; central nerve, a system disorder; dementia; Trandem of p domains in a Weak Inward rectif; ng K4 channel; epilepsy; Alzheimer's disease; Parkinson's disease; mutiple sclerosis; depression; amyotrophic lateral sclerosis; progressive supranuclear palsy; mania; Creutzfeldt-Jacob disease; psychiatric disorfer; schizophrenic disorder; Korsakoff's psychosis; anxiety disorder; phale: C lisorder; amnesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a partial h-TREK1 polypeptive uncoded by the h-TREK1 polynucleotide AA200041. AA200039 and AAV28494 are complete h-TREK1 polynucleotide and polypeptide sequences. hereals is a two pore potassium channel, and the gene maps to human proposome 1q32, between the markers D1S237 and W15105. The polynucleotide is sequence of h-TREK1 can be used to diagnose a disease or susceptibility of a disease related to expression or activity of h-TREK-1 polypeptide. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                  Human
                                                                                                                                                                                                                                  04 -DEC - 2000
                                                                                                                                                                                                                                                                                                                                 AAY90356 standard; Protein; 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular, and inflammatory diseases, pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 18; Page 25; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New two pore potassium channel used for, e.g. . reapulmonary, cardiovascular and inflammatory distributes {\bf p}(x)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFIL: ...
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DB; AAZ00041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             depression and schizophrenia, Alzheimer's, stroke, and head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
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                                                                                                                                                                               protein
                                                                                                                                                                                                                                (first entry)
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98EP-0300570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        migraine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 551; DE : L
; Pred. No. 5.7; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and head trauma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       · reatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :'VAL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC TWIK-2 (Tandem of P domains in a Weak Inward rectifying potassium (K+) CC channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as CC targets for developing modulating agents to regulate a variety of CC cellular processes. They may be useful for developing novel diagnostic CC and therapeutic agents for potassium channel associated disorders, CC e.g. central nervous system disorders (e.g. Alzheimer's disease, CC dementia, Parkinson's disease, multiple sclerosis, amyotrophic lateral CC sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jacob CC disease), psychiatric disorders (e.g. depression, schizophrenic CC disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic CC disorders), learning or memory disorders (e.g. amnesia or age-related CC memory loss), neurological disorders (e.g. migraine), obesity, and CC antibodies against them may be further used in screening assays, predictive medicine. The nucleic acids, proteins, protein homologues and CC predictive medicine. The nucleic acids can be inserted into vectors and
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-572183/53.
N-PSDB; AAA37770, AAA37771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        learning disorder; memory disorder; age-related memory loss; neurological disorder; cardiac disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                   127
                                                                                                                                                                                                                                   114
                                                                                                                                                                                           72
                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                         Local Similarity
GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSA 352
                                                                                                                                   LAGVGDQLGTIFGKGIAKVEDTEIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI
                                                                                                                                                                                                                 IIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents the human TWIK-2 protein of the
                                                                                                                                                                                       vaitgnqt--fnnwnwpnamifaatvittigygnvapktpagrlfcvfyglfgvpl---c
                                 egwnyieglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
                                                                         EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI
                                                                                                               ltwi-salgkffggrakrlgqfltkrgvslrkaqitctvifivwgvlvhlvippfvfmvt
                                                                                                                                                                                                                                                                     iifylaigaaifevleephwkeakknyytqklhllkefpclgqegldkilevvsdaagqg
                                                                                                                                                                                                                                                                                                                                                     105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as gene therapy vectors, to express TWIK protein, to detect TWIK modulate TWIK activity, and screen for drugs or compounds that ate TWIK activity. Host cells may be used to produce non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                  499
                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                   Score 420; DB 21;
Pred. No. 9.4e-37;
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                 120;
                                                                                                                                                                                                                                                                                                                                                                                       Length 499;
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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acid-sensitive potassium channel 2), a novel member of the 2P domain potassium channel family that also includes TW K-1 (see AAV79673) and TASK1 (see AAV79674). TASK2 is a unique potas ium transport channel that is regulated by external pH, and is predo inantly expressed in kidney and epithelial tissues. The invention clates to: identification of the native renal channel with the properties of TASK2; identification of potent pharmacology that specifically modulates the activity of the TASK2 channel incalizing K+ channels comprising the TASK2 gene has been incally and the generation of mice in which the TASK2 gene has been incall and the invention also relates to diagnostic tests and therapentic methods to: detect
                                                                                                                                                                         New nucleic acid encoding a non-inactivating potassium transport channel, designated TASK, of hypertension or dysfunctions of the kidne.
                                                                                                                                                                                                                                                                                                        09-NOV-1998;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TASK2;
                                                                                                                              The present sequence is that of human TASK2 (TWIK-related
                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                     WPI; 2000-376487/32
                                                                                                                                                                                                                                                           Duprat F,
                                                                                                                                                                                                                                                                                                                                           09-NOV-1999;
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                                                                                                                                                                                                                                                                               (CNRS ) CNRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWIK-related acid-sensitive K+ chann: 2 human;
                                                                                                                                                                                                                         AAA27747
                                                                                                                                                   Fig 14a; 91pp; English.
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99US-0436265.
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
77
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
190..2:
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                                                                                                                                                                                                                                                            Lazdunski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "transmembrane domain T2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "transmembrane domain T1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain"
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 105;
24-JUL-1998;
07-AUG-1998;
25-AUG-1998;
09-SEP-1998;
29-SEP-1998;
                                                                                                                                                                                                                                                                                                                            Human protein; hydrophobic domain; nutritional source; haematopoiesis; cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; osteoporosis; osteoparthritis; periodontal disease; asternation; osteoporosis; osteoparthritis; periodontal disease;
                                                                                                                                                                                                                                                                         nervous system disorder; Alzheimer's disease; Parkinson's disease
Huntington's disease; liver fibrosis; lung fibrosis; reperfusion
systemic cytokine damage; tissue differentiation; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreas and/or liver dysfunctions that may arise from mutations the TASK2 gene; protect against tissue rejection in kidney, pancr and liver transplants; and identify potential drugs capable of modulating TASK2 activity.
                                                                                                                                                                   WO200005367-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein clone HP10538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY94875 standard; Protein; 499
                                                                                                   22-JUL-1999;
                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                  coagulation disorder; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and treat human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iifylaigaaifevleephwkeakknyytqklhllkefpclgqegldkilevvsdaagqg 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-ssphs----rkalqvkgstaskdvnifsflskkeety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             egwnyleglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ltwi-salgkffggrakrlgqfltkrgvslrkaqitctvifivwgvlvhlvippfvfmvt 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI 233
                                                                                                                                                                                                                                                 shock; sepsis;
                                                                                                                                                                                                                                   therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
 98JP-0208820.
98JP-0224105.
98JP-0238116.
98JP-0254736.
98JP-0275505.
                                                                                                  99WO-JP03929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension and diseases associated with kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -kvsmf-----vevhkaikkrrrr--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%;
                                                                                                                                                                                                                                                 ischaemia; reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 420;
Pred. No. 9.
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.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120;
                                                                                                                                                                                                                                                 injury; arthritis; tumour;
                                                                                                                                                                                                                                                                  inflammatory condition;
                                                                                                                                                                                                                                                                                                               Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391
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                                                                                                                                                                                                                                                                                 stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                               injury;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hydrophobic domains. The DNA sequences can be the day a probe or as a genetic marker. The protein can also be used as a marker, and to identic disorders. The DNA and protein also be used as potential genetic disorders. The DNA and protein also be used as protein a genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAGA )
(PROT-)
                                                                                                                                                                                                                                                                   inhibitors or agonists of receptor/ligand interactions. They are used treat inflammatory conditions such as septic shock, sepsis, ischaemia reperfusion injury, arthritis, and nephritis. They can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nutritional sources or supplements. The proto exhibits cy proliferation, cell differentiation activities and induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 245-247; 351pp; English.
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                          prevent tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kato
 186
                                             127
                                                                  174
                                                                                                             114
                                                                                        72
                                                                                                                                   12
                                                                                                                                                       54 VVLYLIIGAAVEKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAG
                                                                                                                                                                                         Local Similarity
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                                          IIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents
egwnyieglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
                                                                 LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI
                                                                                                                                 \verb|iifylaigaa| if evleephwkeakknyytqklhllkefpclgqegldkilevvsdaagqg|
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                     EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGAMI CHEM RES CENT
                                                                                                                                                                             Conservative
                                                                                                                                                                                        20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a human protein of .
                                                                                                                                                                             62;
                                                                                                                                                                                        Score 420; DB 21:
Pred. No. 9.4e-37:
                                                                                                                                                                             Mismatches
                                                                                                                                                                             120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be tak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exhibits cytokine,
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                                                                                                                                                                                                 Length 499;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a probe or as a
ker, and to identify
                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production of
                                                                                                                                                                            Gaps
                                                                  233
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GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSA

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The present sequence represents tandem pore domain weak inward potassium (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4, TW
                                                                                                                                                                                                                                                                                                               New tandem pore domain weak inward rectifying potassium ion (TWIK) channel nucleic acids and proteins, useful in assays for identifying candidate compounds which are potential pesticides or therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB31805 standard; Protein; 361
                                                                                                                                                                                                                                                                                 Claim 5; Page 87-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Francis-Lang HL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1999;
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235..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SB,
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Jeschke P;
                     invertebrate for screening
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                                                                                                                                                                                                                             TWIK3, TWIK4
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Best Local
                                       New tandem of P domains in a weak inward rect, ying proteins and genes for e.g. developing theraphatic channel associated disorders, e.g. central nervous disorders
                                                                                                WPI; 2000-572183/53.
N-PSDB; AAA37766, AA
                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                          Creutzreldt-Jacob disease; psychiatric disord. : schizophrenic disorder; Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia; learning disorder; memory disorder; age-related memory loss; obesity;
                                                                                                                                                                                                                                                                                                                                                        amyotrophic lateral sclerosis; progressive sur anuclear palsy;
Creutzfeldt-Jacob disease; psychiatric disord. : schizophrenic
                                                                                                                                                                                                                                                                                                                                                                                Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; dementia; Tandem of P domains in a Weak Inward rectifying K+ channel; epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prognosis
                                                                                                                                        Curtis
                                                                                                                                                                                        01-MAR-1999;
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                                                                                                                                                                                                                                          08-SEP-2000.
                                                                                                                                                                                                                                                                  WO200052164-A2
                                                                                                                                                                                                                                                                                                                   neurological disorder; cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TWIK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY90354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY90354 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAGGSDIE- LDFYKPVVWFWILVGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alverlliptvw-----llqwlnsklghlyqplrir >hlaiivlvllvfflllp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVGDQL--GTIFGKGIAKVEDTFIKWNVSQ-----TKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alenatse-pnwsfgqsfffastvittigyghvtplsrngk tcmfyavvgipltlvlls
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mflcsgaavfsyfeapeeralrvklgtavqkflvsnpnvtdadleeliveivrannrgvs 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACYNS% LDELIQQIVAAINAGII 115
                                                                                                                                        RAJ;
                                                                                                                                                               MILLENNIUM PHARM INC
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                                                                                                   AAA37767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. central nervous system,
                                                                                                                                                                                                                                                                                                                   disorder;
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                                               potassium channel
agents for potassium
system, psychiatric
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                                                                                                                                                                                                                                                                                                                                                                       mania;
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Claim 8; Fig

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148pp; English

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RESULT 15
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Best Local :
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(CNRS ) CNRS CENT NAT RECH SCI
                                     08-FEB-1996;
                                                                        08-FEB-1996;
                                                                                                                14-AUG-1997.
                                                                                                                                                     FR2744730-A1
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                   TWIK-1 potassium channel protein
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                                                                                                                                                                                                                                                                                                                                                                                                     AAW23397 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ppllfshmegwsytegfyfafitlstvgfgdyvigmnpsqryplwyknmvslwilfgmaw 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGFLLAGVGDQLGTIFGKGI----AKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVAL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt lllaylaylalgtgvfwtlegraaqdssrsfqrdkwellqnftcldrpaldslirdvvqa}
                                                                                                                                                                                                                          potassium channel; screening; diagnosis; transgenic animal;
of P domains in a Weak Inward rectifying K+; antibody.
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                                     96FR-0001565
                                                                        96FR-0001565
                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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Pred. No. 2e-33;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for modulating activity of TWIK-1 type channe stany also be useful therapeutically, e.g. for control of epileps, arrhythmia, vascular disease, neurodegeneration (particularly of ischaemic or anoxic origin), endocrine or muscular disorders. The cDMA and the vectors can also be used to create transgenic animals (especially knock-out animals) for use as models of TWIK-1 related diseases. Analysis of the sequence of the TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies can be used to detect TWIK-1 channels and for inhibiting or activating the channels in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channels consisting of 4 transmembrane segmc 3 and two P domains, being only weakly rectifying. The CDNA, vect 3, the cells express TWIK-1 type channels and the protein are use 50 compensate for deficiency of potassium channels in varias tissues. Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a protein commising a potassium channel with the properties of a TWIK (Tandem of P downins in a Weak Inward rectlifying K+) 1 channel. This is the first wher of a new family of channels consisting of 4 transmembrane segme and two P domains, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding new potassium channel designated TWIK-1 -useful for treating channel deficiency diseases, screening for active agents and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Figure 1b; 37pp; French
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Lesage F, |
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                                   FAAVLSMIGDWLRVISK-----KTKEEVGEFRAHAAE 316
                                                                                                                                                            LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRI; LI
                                                                                                                                                                                                              1997-427773/40.
DB; AAT64960.
mlvvletfce-lhelkkfrkmfyvkkdkdedqvhiie
                                                                                                                                           ftllfltavvgritvhvtr--rpvlyfhirwgfskgvvai avllgfvtvscfffi--p
                                                                    aavfsvleddwnflesfyfcfislstiglgdyvpgegyngkirelykigitcylllglia
                                                                                                          AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDI': LDFYKPVVWFWILVGLAY
                                                                                                                                                                                                                                                                                                                                                            90;
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                                                                                                                                                                                                                                                                                                                                                        18.0%; Score 376.5; EB 1 32.5%; Pred. No. 2.8e-32; tive 62; Mismatches 10H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guillemare E,
                                                                                                                                                                                                                                                                                                                                                                                            LB 18; Length 336;
                                                                                                                                                                                                                                                                                                                                                            104;
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                                                                                                                                                                             11--EILFGCVLEVALP
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                                                                                                          284
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Search completed: August 28, 2001, 17:05:47 Job time: 1892 sec

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Title: Perfect score: Sequence:

US-09-503-089A-4 2090

MAAPDLLDPKSAAQNSKPRL.....LNGLTPHCAGEDIAVIENMK 411

protein -

protein search, using sw model

Copyright

GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd

August 28, 2001, 17:06:21; Search time 28.01 Seconds (without alignments) 302.129 Million cell updi

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0

Minimum DB Maximum DB

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length:

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Total number of hits satisfying chosen parameters:

197339 seqs, 20590346 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Issued_Patents_AA: *

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 410; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: NO. 6242217el Compounds
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
RUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                301
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                                                                                                                                241
                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                                                      ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGHOIAVIENMK
                                                      Conservative
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US-09-111-752-7

US-08-436-900A-4

US-08-637-823B-3

US-08-637-823B-3

US-08-637-823B-3

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US-08-637-823B-3

US-08-637-823B-3

US-08-637-823B-3

US-08-837-077C-4

US-08-837-077C-4

US-08-895-590-4

US-08-466-886-1

US-08-469-617-1

US-08-637-823B-3
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Pred. No. 2.2e
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2.2e-211,
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Sequence 7, Appli
Sequence 4, Appli
Sequence 30, Appli
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Sequence 6, Appli
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Sequence 80, Appli
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SUMMARIES

2000 2000

US-09-236-080-6
US-09-236-080-2
US-09-236-080-2
US-08-749-816-2
US-08-332-312-2
US-08-749-816-4
US-08-749-816-3
US-09-135-021-80
US-09-135-021-80
US-08-677-734A-11
US-08-677-734A-1
US-08-677-734A-1
US-08-677-734A-1
US-08-597-236-13
US-08-597-236-13
US-08-597-236-13
US-08-956-242-4
US-08-956-242-13
US-08-956-242-13
US-08-956-242-13
US-09-351-215-2
US-09-351-215-3
US-09-351-215-3
US-09-351-215-3
US-09-351-215-3
US-09-351-215-3

Sequence

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Best Local Similarity 96.4
                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 107
                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                     Sequence 4, Application US/09236080 Patent No. 6242217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 411
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                                                                                       CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25 NUMBER OF SEQ ID NOS: 6
                                                                                                                                          APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6:
FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Helen Meadows
APPLICANT: Contrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
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ORGANISM: Homo
                    TYPE: PRT
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5. 6242217
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96.4%; Pred. No. 3.66
tive 11; Mismatches
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                                                                                                         Query Match
Best Local (
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Best Local Similarity
                                                                                            Matches
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                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 15 NOV-1996
                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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109 AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGN: SPRTEGGKIFCIIYALLGIP 168
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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                                                           51 FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTF
                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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                                                                                                                                                                                                                                  LENGTH:
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                                FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRF
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                                                                                            Conservative
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Lazdunki, Michel
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THEIR CLONING AND THEIR SEE ESPECIALLY FOR THE SCREENING
OF DRUGS
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                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pausch, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                             166 GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-----QTKIRIISTIIFILF-G
                                                                                                            106
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129 GIPVNGILFAG----LGEYFGRTFEAIYRRYKKYKMSTDMHYVPPQLGLITTVVIALIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295
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                                                                      69 ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI 128
                                                                                                                                                                         50 IFLVVVLYLIIGAAVFKALEQPQE----ISQRTTIVIQKQTFIAQHACVNSTELDELIQQ 105
                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: P-38,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                             9
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                                                                                                        IVAAINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
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Pausch, Mark H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Melanagaster
                                                                                                                                                                                                                                 14.3%; Score 299.5;
25.7%; Pred. No. 6.
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                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                6.1e-23;
ches 151;
                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                    Length 618;
                                                                                                                                                                                                                  Indels
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US-08-332-312-4
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                                                                                              Matches
                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Functional Expression TITLE OF INVENTION: Melanagaster Putative NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: American Cyanamid Company
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3246
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                                                           120 SSNQVSH------WDLGSSFFFAGTVITTIGFGNISPRI GGKIFCIIYALLGIPLFGFL 173
 174 LAGVGDQLGTIFGKGIAKVEDTFIK---
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 CVLFVALPAV---IFKHIEGWSALDAIYFVVITLTTIGFGDYVA------
                                                                                                                                                                                                                                                                                                                                       NAME: Harrington, James REGISTRATION NUMBER: P-REFERENCE/DOCKET NUMBER:
                                 15 TSNEVKKNAATETWTFSSSIFFAVTVVTTIGYGNPVPVTNIGRIWCILFSLLGIPL---T
                                                                                                                                                                                                                             TYPE:
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CITY: Wayne
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Pausch, Mark H.
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                                                                                              Conservative
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                                                                                                            10.5%;
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                                                                                             36;
                                                                                           Score 219; DB 1; Pred. No. 7.4e-15; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                       32,421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
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   -WNVSQT 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-00S
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                              Local
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REGISTRATION NUMBER: 19,763
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                                                                                                      11 SAAQNSK-PRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLIIGAAVFKALE 69
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 15-NOV-1996
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                                                                                                                                                                                                                                                                                                                      LENGTH:
   HPEELKRREKAI ----
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                                                                     SMEENSKIOMLSATSKOKKVATORSLINKYHLGPLALHTGLVLSCVTYALGGAYLFLSIE 63
                                                                                                                                            84;
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                                                                                                                                                              Similarity
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230 South Fifteenth Street,
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VENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
VENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Romey, Georges
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: 19
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----REFQDLKQQFMGNITSGIENSEQSIEIYTKKLI 108
                                                                                                                                                                                                                                                                                                                                                                                                                            989.6351P
                                                                                                                                          Score 184.5; DB 3
Pred. No. 3.9e-11;
4; Mismatches 114
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                                                                                                                                                                           DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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REGISTRATION NUMBER: 19
REFERENCE/DOCKET NUMBER:
                             52 LVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIACHACVNSTELDELIQQIVAAIN 111
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ITLLVFNLIGAGIFYLAE----TQNSSESLNENSEVSK--CLHNLPIG---GKITAEMK 93
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                                                                         Similarity
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230 South Fifteenth Street,
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Barhanin, Jacq
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PC-DOS/MS-DOS
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THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
OF DRUGS
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Best Local Similarity
Matches 92; Conserv
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SEQ ID NO 2
LENGTH: 676
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EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
FILE REFERENCE: 2323-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 80
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                                                                                      FGDYVAGGSDIEYLDFYKPVVWF-----WILVGLAYFAAVLSMIGDW--LRVISKKTK
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CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 581
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APPLICANT: Keating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KY
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
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SPKPKKSVVVKKK---KFKLDKDNGVTPGEKMLTVPHIT
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                                                                   ALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSS:::KIYIR---KAPRSHTLLSP
                                                                                                    -LRVISKKTKEEVGE-----FRAHAAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106.5; ; Pred. No. 0.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                 ENTED 383
. ---PP 353
                                                                                           WIANVTAEFKETRRRLSVEI
                                                                                                                                                                    :::LVGLAYFAAVLSMIGDW-
                                                                                                                                                                                                    AVNESGRVEFGSYADALW
                                                                                                                                                                                                                                                                                                                                          ISIIDLIVVVASMVVLCV
                                                                                                                                                                                                                                                                                                                                                                        ---LGSSFFFAGTVITTI 143
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                                                                                                                                                                                                                                       ·---HIEGWSALDAIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           indels 145;
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RESULT 11 US-08-677-734A-11

Sequence 11, Application US/08677734A Patent No. 5871919
GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Brant, Steven R. Yun, Chris C.H.

Donowitz, Mark

US-08-677-734A-12

Million.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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333
                                        316 EWTANVTAEFKET 328
                                                                                                                                                                                                                  241
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                                                                                                                                                                                                                                                                                                                                                                                       146 GNISPRTEGGKIFCIIYALL------GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTF 196
                                                                                  273 TRFTKHVRIIEPGFVFVISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISEQSATTV 332
                                                                                                                                                                                                                                                                                                      197 IKWNVSQTKIRIISTIIFILFGCVLFVALPA------VIFKHIEGWSALD--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FORGLS, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 10-JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                      87
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RYTMKMLASGAET 345
                                                                                                                             GDW---LRVI----
                                                                                                                                                                       TVVLYNVFESFVTLG-GDAVTG-----VDCVKGIVSFFVVSLGGTLVGV-IFAFLLSLV
                                                                                                                                                                                                                  --AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMI 292
                                                                                                                                                                                                                                                            ----MGELKIGLLD----FLLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAV 220
                                                                                                                                                                                                                                                                                                                                            GNL-----GTI--LLYAVIGTIWNAATTGLSLYGVFLSGL------ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVTFKWHHVQDPYIIALWILVASLAKIVF-----HLSHKVTSVVPESALLI------ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVMKWKTVSTIFLVVVLYLIIGAA--VFKALEQPQEISQRTTIVIQKQTFIAQHACVNS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VLGLVLGGIV---WAADHIASFTLTPTLFFFYLLPPIVLDAGYFMPNRLFF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGSSFFF-----AGTVI-TTIGF 145
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1300 I Street, N.W., Suite 700
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VENTION: Cloning, Tissue Distribution, and
VENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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10-JUL-1996
ON: 435
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                                                                                                                          ---SKKTKEEVGEFRAHAA 315
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Brant,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                             223 TVVLXNVFQSFVTLG-GDKVTG------VDCVKGIVSFF CSCGTLVGVV-FAFLLSLV 274
                                                                                                                                                                                                                      137 SNL-----GSI--LLYAVVGTVWNAATTGLSLYGVFLSGI-----
                                                                                                                                                                                                                                                            146
275 TRETKHVRVIEPGEVETISYLSYLTSEMLSLSSILAITECS CCORYVKANISEQSATTV 334
                                    293 GDW---LRVI-----
                                                                                                                                                                                197 IKWNVSQTKIRIISTIIFILFGCVLFVALPA---------VIFKHIEGWSALD---
                                                                                                                                                                                                                                                                                              88
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                                                                                                                                                                                                                                                                                                                                                                                         39 INVMKWKTVSTIFLVVVLYLIIGAA--VFKALEQPQEIS,k :IVIQKQTFIAQHACVNS 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fordis, Jean B. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/677,734A FILING DATE: 10-JUL-1996
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ZIP: 20005-3315
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                                                                                                                                                                                                                                                        GNISPRTEGGKIFCIIYALL------GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTF 196
                                                                                                                                                                                                                                                                                                                                                                    IVTFKWHHVQDPYIIALWVLVASLAKIVF------HLS.HK:.SVVPESALL------ 87
                                                                                                            --AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMI 292
                                                                                                                                                                                                                                                                                                                                TELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGSSFFF-----AGTVI-TTIGF 145
                                                                                                                                            ----MGELKIGLLD----FLLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAV 222
                                                                                                                                                                                                                                                                                            -----IVLGLVLGGIVL--AADHIASFTLTPTVFFFYLLPPIVLDAGYFMPNRLFF 136
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ilarity 19.8%;
Conservative 55
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Donowitz, Mark
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N: 435
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                                  -SKKTKEEVGEFRAHAA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 832;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 151;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                              127
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                              223 VALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI----
                                                               163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 EWTANVTAEFKET 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                                                                              87 LLIVLGLVLGGIVWAA----
                                                                                                                                                                                                                        52 LVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAIN 111
                                                                                                                                                                                                                                                            Local Similarity
les 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 10-JUL
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DAVTVVLYNVFESFVAL---
                                                              YGVFLSGLMGDLQIGLLDFLLFGSLMAAVDPVAVL--AVFEEVHVNEVLFIIVFGESLLN 220
                                                                                            FGFLLAG-VGD-QLG----TIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG-CVLF 222
                                                                                                                              AGYF - - - - MPNRLFFGNLGTILLYAVVGTVWNA - - - - - -
                                                                                                                                                            AGIIPLGNSSNQVSHWDLGSSFFFA--GTVITTIGFGNISPRTEGGKIFCIIYALLGIPL 169
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Donowitz, Mark
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                         4.68;
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                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                        Score 96.5; DB Pred. No. 0.24; 9; Mismatches
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al Analysis Of The Hu
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 -GGDNVTGVDCVKGIVSFFVVSLG 260
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                                                                                                                              ----ATTGLSL
                                                                                                                                                                                                                                                                                          Length 834;
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                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FITLE OF INVENTION:
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| 261 GTLVGVV-FAFLLSLVTRFTKHVRIIEPGFVFIISYLSY: ; EMLSLSAILAITFCGICC 319
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                                                                                                                                                                                       52 LVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAC
                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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VALPAVIEKHIEGWSALDAIYFVVITLTTIGFGDYVAGC:
                             YGVFLSGLMGDLQIGLLDFLLFGSLMAAVDPVAVL--Ai
                                                            FGFLLAG-VGD-QLG----TIFGKGIAKVEDTFIKWNVS
                                                                                           AGYF----MPNRLFEGNLGTILLYAVVGTVWNA----
                                                                                                                         AGIIPLGNSSNQVSHWDLGSSFFFA--GTVITTIGFGN1
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5871919
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1300 I Street, N.W., Suite 700
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                   Score 96.5; DI Pred. No. 0.24; 3
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                               THUNEVLETIVEGESLIN 220
YLDFYKPVWFWI - - - -
                                                            RIISTIIFILFG-CVLF 222
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PRIOR APPLICATION UMBER: EP 95201669.9
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
NAME: Fanucci A., Allan
NAME: Fanucci A., Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/08597236 Patent No. 5733765 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       Query Match 4.6%; Score 96; DB 1; Length 473; Best Local Similarity 22.8%; Pred. No. 0.12; Matches 47; Conservative 33; Mismatches 52; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTI
TITLE OF INVENTION: EXOPOLYSACCI
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CORRESPONDENCE ADDRESS:
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STATE: New York
COUNTRY: U.S.A.
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221 DAVTVVLYNVFESFVAL----
                                       203 OTKIRI-ISTIIFILFGCVLFVALPA 227
                                                                                                                                                                 310 VEKVV------SSDYASSWQYVPFFMLSMLFSSFSDFFGTNYIA-----AKQ 350
                                                                                                                                                                                                         103 IQQIVAAINAGIIPLGNSSNQVSHWD------LGSSF--FFAGTVITTIGFGNISPR 151
                                                                                                                                                                                                                                                        280 KSKYYSDVFHYLATFLLLGTSAFMIVLKP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 --LVGLAYFAAVLSMIGDW---LRVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 426
                                                                                                                                                                                                                                                                                           43 KWKTVSTIFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDEL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                   TEG------GKIFCIIYALLGIPLFGFLLAGVGDQLG--TIFGKGIAKVEDTFIKWNVS 202
QIKWRIFISNLLIVLAQILCLFYLPS 432
                                                                                 TKGVFMTSIYGTIVCVLLQVVLLPIIGLDGAGLSAMLGFLTTF---LLRVKDT-QKFVVI 406
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Search completed: August 28, 2001, 17:06:22 Job time: 526 sec

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Maximum Match 100%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Oy 285 FAAVLSMIGDWLRVISKKTKEEVGEFRAHAAE	Qy 227 AVIEKHIE-GWSALDAIYEVVITLTTIGEGDYVAG-GSI	Qy 169 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIK: (ST11FILFGCVLFVA	Oy 109 AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGN1SPRTEGGKIFCIIYALLGIP	Qy 51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQXQT' : ACCUNSTELDELIQQIVA	Query Match 18.0%; Score 376.5; L.7. Best Local Similarity 32.5%; Pred. No. 5.3e Matches 90; Conservative 62; Mismatches;	A;Reference number: \$65566; MUID:96183184 A;Reference number: \$65566 A;Rocession: \$65566 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-336 <les> A;Cross-references: EMBL:U33632; NID:g1086490; P (1) AB01688.1;</les>	, Arr	i, =	ALIGNMENTS	30 215.5 10.3 335 2 S44635 31 212 10.1 485 2 T24201 32 209.5 10.0 586 2 T21583 33 206.5 9.9 660 2 T21551 34 205 9.8 700 2 T237364 35 204.5 9.8 576 2 T43363 36 204.5 9.8 576 2 T43363 37 204.5 9.8 576 2 T43363 38 202.5 9.7 769 2 T27550 39 199.5 9.7 769 2 T23770 40 196.5 9.4 681 2 T19429 40 196.5 9.4 681 2 T19429 41 194.5 9.3 381 2 T43393 42 192.5 9.3 569 2 T43393 43 189 9.0 504 2 T223746 44 184.5 8.8 600 2 T24626
	SI · LDEYKPVVWEWILVGLAY 284 SING	IIFILFGCVLFVALP 226 :: :	TEGGKIFCIIYALLGIP 168 SDGGKAFCIIYSVIGIP 143	:ACVNSTELDELIQQIVA 108 : : : : : : : : : : : : : : : :	Length 336; Indels 17; Gaps 9;	CLITAIN V(+) Channel with a nove	Bar	*text_change 05-Nov-1999		f22b7.7 protein - hypothetical prote potassium channel potassium channel hypothetical prote

probable potassium channel chain n2P38 - Caenorhalditis elegans C.Species: Caenorhabditis elegans C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change C;Accession: T43509 R.Wang, Z.W.; Salkoff, L. submitted to the EMBL Data Library, August 1998 A.Description: Potassium channels in C. elegans. A;Reference number: Z22450

21-Jan-2000 #text_change 21-Jan-2000

RESULT T43509

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MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE

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R;Murray, J.; Wohldmann, P.; O'Neal, D.

submitted to the EMBL Data Library, September 1997

A;Description: The sequence of C. elegans cosmid F34D6.

A;Reference number: Z21153

A;Accession: T32347

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-336 <MUR>
A;Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.

A;Experimental source: strain Bristol N2; clone F34D6

C;Genetics:
A;Emperimental Source: STAD6.3

A;Map position: 2

A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-329 <WAN>
A;Cross-references: EMBL:AF083652; PIDN:AAC32863.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTEL 99
DLIIFCTGWGGLLIFGGAFWESSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQ
                                   TIIFILFGC-VLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---D 263
                                                                                                        RTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIS
                                                                                                                                                                               CVNSTELDELIQQIVAAI -- NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISP 150
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                                                                       MTDAGKVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSS
                                                                                                                                            MSNA-DYEILEATIVKSVPHKAGY------QWKFSGAFYFATTVITTIGYGHSTP 108
                                                                                                                                                                                                                   MKRQNIRTLSLIVCTLTYLLVGAAVFDALETENEILQVRGLGEPRKLVQRVREKLKTKYN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCMLYALAGIPLGLIMEQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSSDLIIFCT 163
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                                                                                                                                                                                                                                                                                            94;
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33.2%;
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Pred. No. 1
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No. 2.7e-20;
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submitted to the EMBL Data Library,
A;Reference number: Z19703
A;Accession: T23182
A;Status: preliminary; translated f:
A;Molecule type: DNA
A;Residues: 1-38 <MIL>
A;Cross-references: EMBL: Z75543; PII
A;Cross-references: EMBL: Z75543; PII
                                                                                                                                             hypothetical protein K01D12.4 - Caenorhabditis c ... (;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-15.50 C;Accession: T23182 R;Dobson, R.
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R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; st., ch, M.H. Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, st. st. Price, L.A.; Title: ORKI, a potassium-selective leak channe st. two po. A;Reference number: Z17770; MUID:97075152

A;Accession: T13807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    potassium channel protein - fruit fly (Drosophila relanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-199; 'ext_change
A; Experimental source: C; Genetics:
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A; Residues: 1-1001 <GOL>
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                                                                                                                                                                                                                                                                                                                                                                                              269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVAAINAGIIPLGNSSNQVSHWDLGSSEFFAGTVITTIC ( SPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEYV-FFSLV---FILFGLTVISAAMNLL--VLRFLTMN1855
                                                                                                                                                                                                                                                                                                 VGYLRRMLN-ELY
                                                                                                                                                                                                                                                                                                                                 FKETRRRLSVEIY 337
                                                                                                                                                                                                                                                                                                                                                                FV--IVWF--IFSLGYLVMIMTFITRGLQ--SKKLAYLF
                                                                                                                                                                                                                                                                                                                                                                                  GIPVNGILFAG----LGEYFGRTFEAIYRRYKKYKMST:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-.
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                  clone K01D12
                                                                                                                                                                                                                                                                                                 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.6%; Score 325; 28.8%; Pred. No. 2
                                                                                                                                 Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                PIDN:CAA99871.1
                                                                                   from GB/EMBL/DDBJ
                                                                                                                                  June
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                                   SEPLA: CN00023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . WWFOLGLITTVVIALIPG
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                                                                                                                                                                               .ext_change 15-Oct-1999
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                                  CESP: K01D12.4
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RESULT 6
T19860
T19860
Rypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19860
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                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-334 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z19188
A; Accession: T19860
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A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2
                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                             :Map position: :
:Introns: 34/1;
                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:270266; PIDN:CAA94204.1; Experimental source: clone C40C9
                                                                                                                                                                                                                                                                                                              Gene: CESP:C40C9.1
                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated
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                                                                                                107
                              166 GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----wnvSQTKIRIIS-TIIFILFG
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                                                                 65
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                                                                                                                                                            50 IFLVVVLYLIIGAAVFKALEQPQEISQRTTIV---IQKQTFIAQHACVNSTELDELIQQI 106
                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 DERIAIDNRMADYQKVYCKHKPLNECDFEEMVRFISDGATSGLL---NSRSRFDH--LG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLG----IPLFGFLLAGVGDQLGTIFGK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLIIGAAVFKALEQPQEI
GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV--
                                                                                              VAAINAGIIPLGNSSNQVSH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                LILSTFTYLLFGAMVFDKLE----SEKDTWVRDEIERITDRLKHK-YNFSERD----LHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTLGACFFYCLSNVSSIVVRQLLNWM----IKKMDVKV-EDRSFLC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILVGLAYF-----AAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVLITASAGIYSVVENWNYIDSLYFCFISFATIGFGDYVSNQQDVTRMSPDLYRFVNFCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLFFSATVISTIGFGTSTPRTHLGRFITIVYGVVGCTCCVLFFNLFL----ERLVTGMSY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQRTTI----VIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGS
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                                                             FEAIAIKSIP-----QQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF
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                                                                                                                                                                                                90;
                                                                                                                                                                                                                                                                                 60/2;
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                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                             98/1; 145/3; 160/3; 181/1;
                                                                                                                                                                                                            13.7%;
28.7%;
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Pred. No. 7.6e
80; Mismatches
                                                                                                                                                                                                              Score 286.5; DB 2; Pred. No. 1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                              from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              March
                                                                                                                                                                                                Mismatches
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1.6e-16;
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                                                                                                                                                                                                                                                                             204/1;
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                                                                                                                                                                                                                             Length 334;
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                                                                                                                                                                                                                                                                             252/2;
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                                                                                                                                                                                                                                                                             279/2;
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                                                                                                                                                                                              Gaps
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RESULT
T43394
A; Reference number: Z2;
A; Accession: T43394
A; Status: preliminary;
                                                                                                        potassium channel chain n2P18 homolog C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
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A;Description: Postssium channels in C. elegans
A;Reference number: Z22450
A;Accession: T43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable potassium channel chain n2P20 - Caenorhabdinis
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-20-1 text
                               A; Description: Potassium channels A; Reference number: Z22479
                                                                             C; Accession:
R; Kunkel, M.1
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R; Wang, Z.W.; Salko
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                                                              submitted to the EMBL Data Library,
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A; Residues: 1-364 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAAINAGIIPLGNSSNQVSH-WDLGSSEFEAGTVITTIGEGGHESPRTEGGKIECIIYALL 165
                                                                                                                                                                                                                                                                                   FILIGLAVFSACVNLL-
                                                                             M.T.; Salkoff, L.
                                                                                                                                                                                                                                                                                                                                                                CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYY--AGGSDIEYLDFYKPVVWF
                                                                                                                                                                                                                                                                                                                                                                                                                                   GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG
                                                                                                                                                                                                                        LERFTRNSLVDSQI
                                                                                                                                                                                                                                                    YDKFQRATSVKRKL
                                                                                                                                                                                                                                                                                                               WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHA/ WTANVTAEFKETRRRLSVEI 336
                                                                                                                                                                                                                                                                                                                                              ----IVSGTYMEHTIEKWSIEDAYYECMITESTIGEGDI.VPLQQVNALQDQDLYVEATIM
                                                                                                                                                                                                                                                                                                                                                                                                              GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LILSTFTYLLFGAMVFDKLE----SEKDTWVRDEIERLTE-LKHK-YNFSERD---LHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LERFTRNSLVDSQI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVLEVALPAVIFKHIEGWSALDAIYEVVITLTTIGFGD:
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                                                                                          T43394
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   from GB/EMBL/D:
                                               in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 286.5;
                                             August 1998
n C. elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                        21-Jan-20
                                                                                                                                                                                                                                                                                     -VLGFMASNADEVTA - - -
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No. 1.1e-1
                                                                                                                                        Caenorha
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                                                                                                            #text_change
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                                                                                                                                         elegans
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                                                                                                             21-Jan-2000
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type: mRNA

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A;Reference number: Z20027
A;Reference number: Z20027
A;Accession: T25392
A;Accession: T25392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-393 < WIL>
A;Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1
A;Cross-references: clone T28A8
 밁
                                Q
                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЬ
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A; Introns: 73/1; 112/3;
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A; Cross-references: EMBL: AF083650; PIDN: AAC32861.1
                                                                                                                                                                                                                                                                                    A; Gene: CESP: T28A8.1
                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, March 1997 A; Reference number: Z20027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T25392
                                                                                                                                                Query Match 13.3
Best Local Similarity 27.5
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211
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                                                                     ---TIIFILFGCVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL 267
EMRESGIGOHVVEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDY -- NWTYMTAL 121
                                  --KQTFIAQHACVNST--ELDELIQQIVAAINAGII-----PLGNSSNQVSHWDLGSSF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TDNDLLETLIREE 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSEREVLPPLLKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQELTP-----CRRTLSVNHL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKGCKMLWRFFLK-----STRVVSKDLSNKISEAADNIEEGTTAITPSAEKTENNDDDL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKGIAKVEDTFIKWNVSQTKIRIIS -----------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TILTTFQKTFKGLLPLIILVAYTLLGAWIFWMIEGENE---REMLIEQQK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVSTIF-----LVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDPEEDPENNKKSFDAV--ISRMNWSKRGLYYLLPDSQKKELAKQSEKKMGRKSIKIQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PIVGVLLLIGLSLVSTVMTLIQQQIEALASGMKDNIDQEYARALNEAREDGEVDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHA-----AEWTAN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSFPISGLLLITVIWVIFCAVLFTFLEEWDFGTSLYFTLISFTTIGFGDILP--SDYDFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --ERDELIRRTVYKINQLQIKRQRRLMTAEEEYNRTAKVLTTFQETLGIVPA--DMDKDI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STELDELIQQIVAAIN------AGIIPLGNSSNQVS
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                                                                                                                                                                                                                                           179/2; 209/3; 287/2; 310/3; 364/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 279.5; DB 2; 23.5%; Pred. No. 5.6e-15; ative 70; Mismatches 133;
                                                                                                                                                                  13.3%;
                                                                                                                                                  51;
                                                                                                                                                Score 279; DB 2;
Pred. No. 5.1e-15;
1; Mismatches 106;
                                                                                                                                                                                   Length 393;
                                                                                                                                                Indels
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hypothetical protein x39B6B.f [imported] - Caenoriabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45032
R;Wilson, R; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burraser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.;
B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.
Nature 36B, 32-3B, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
A;Reference number: S43531; MUID:94150718
A;Accession: T45032
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A; Introns: 47/2; 8
A; Note: Y39B6B.f
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A; Residues: 1-392 <WIL>
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Best Local
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  332
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                                                                                                                                                                                                                                                                                                                                                            58
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YLMGGLCCMMLFLATLYD 349
                                                                           LDPKSAAQNS----KPRLSFSSKPTVLAS----RVESD : INVMKWKTVSTIFLVVVLY 57
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                                    WILVGLAYFAAVLSMIGD
                                                                                                                                                         SAIVARMREPSHKLRGLLNQRLGHLF-
                                                                                                                                                                                                                                                       IPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGK1FCIIYALLGIPLFGFLL 174
                                                                                                                                                                                                                                                                                                                                                                                                   LEPRTSAHQSSLYPVEPKMAIAKEMSFYSDQKIPKFHFFFSLKISKLKPAKNRY------ 117
                                                                                                                                                                                                                                         IWMDRNLTSDPNWTFGQAFFFAGTLISTVGYGRVSPRTEYGKLFTILYCVIGIPLTLALL
                                                                                                                                                                                                                                                                                                                     -----FSRIEYPLEKIEREAYLDYQNQWRDRLIQLDIDESEIDKLFLNIREAALNG-- 168
                                                                                                                                                                                                                                                                                                                                                            LIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQ--HACVNSTELDELIQQI-VAAINAGI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLREKCSKQ--KYSVISSKDDKNKEGDLNLDHLENYIS (1 IFLIVAILLSYITFGAVVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82/2; 106/3; 151/1; 220/1; 260/3: 170/3
                                                                                                                                                                                                ---GDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.0%; Score 271; DB 2; Length 392; 25.8%; Pred. No. 2.3e-14; Live 65; Mismatches 109; Indels
                                      294
                                                                                                                                                         · · FVNHIQLIHVGV-VFASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
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M.; Jo
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C;Species: Caenornawatta C. C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C;Accession: T15584
R;Favello, T.
submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Cibrary C;Accession: The sequence of C. elegans cosmid (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Rolecule type: DNA
A; Residues: 1-522 <WIL>
A; Cross-references: EMBL: Z70036; P
A; Cross-references: clone T01B4
A; Molecule type: DNA
A; Residues: 1-325 <FAV>
A; Cross-references: EMB
                                                A; Accession: T15584
A; Status: preliminary; translated
                                                                                   A; Description: The sequence of A; Reference number: Z18373
                                                                                                                                                                     hypothetical protein C24A3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t.C;Accession: T15584
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A; Introns: 95/3; 142/1;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Wilkinson,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                        371 VNHLTSEREVL
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                                                                                                                                                                                                                                                                                                                       NEHDSCQIEAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KRCLELITKTFIQRSDEERGEGWRWDFWNSVFFSATIFTTIGYGNLACKTNLGRI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LILIILGYACLGGYMFQALEYDQQQLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VENQYMWALELIDQKYQEKLKQDMYDEDEKKADKNDMHFSKKEPVRGPRILLQDLLRGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----W-LRVISKKTKEEVGEFRAHAAEWTANVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAKV-----EDTF--IKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTIYGMIGIPLMLFVLKNFGELCVKWAKKIQFNVQQCLKKCFGRKQKRASSLASITSKE
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                                                                                                                                                                                                                                                                                                                                                                                             LKISGGRRSSSDASSVITEASDEDTRHFKVGRAILAEAFAPDERASNHGTQLNSC--TVS
                                                                                                                                                                                                                                                                                                                                                                                                                                AEFKETRRRLS-----VEIYDKFQRATSVKRKLSAEL-----AGNHNQELTPCRRTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLTAFYFFFVSLSTIGFGDIVP------DHPRTACALFVLYFIGLALFAMVYAILQER 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDELIQQIVAAINAGIIPLGNSS-NQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
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EMBL:U40424; NID:g1065542; PID:g1065543; PIDN:AAA81455.1; CESP:C24A3
                                                                                                                                                                                                                                                                                                                                                            381
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23.7%;
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                                                        from
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Pred. No. 3.5e-14;
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                                                        GB/EMBL/DDBJ
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                                                                                                                                                                                    20-Sep-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                              C24A3
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hypothetical protein F19D8.1 - Caenorhabditis elc.; C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-199...
C:Accession: T21118
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submitted to the EMBL Data I
A;Reference number: 219377
A;Accession: T21118
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A; Introns: 21/1;
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A: Tntrons: 31/1;
                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z78541; PIDN:CAB01740.1: G. PDB:GN00028; CESP:F19D8.1
A;Experimental source: clone F19D8
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-452 <WIL>
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Matches
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Best Local Similarity
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                                               146 VLFSFTILTTIGYGNVTPHTQQCKVFLMIYGAFGIPLFLITIADLGRFSKTAIMALVQKV
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                                                                                                                                                VIOKOTFIAQHACV-NSTELDELIQQIVAAINAGIIPLA: ----NSSNQV--SHWDLGSS 132
                                                                                                                                                                                                                 RVESDSAINVMKWKTVSTI-----FLVVVLYLIIGAAVFKALEQPQEI----SQRTTI
            EDTFIKWNVSQTKIRIISTI---IFILFGCVLFVALPAVIFKHIEGW---
                                                                              FFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKV 192
                                                                                                                 MNLKKDVIAKLATTENVAEINEHLRMFLRNISNLHISLDNYLIENEPTQIVPKRWTFPSS
                                                                                                                                                                                 KLKCNSKCAWMKFRNVLRIALGHLALYCFVVCYVFAGAWVFWJLEGENETELHDKQREYA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYAH LGIPLFGFLLAGVGDQLGTIF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ERDELIRRTVYKINQLQIKRQRRLMTAEEEEYNRTAKVUTTYQETLGIVPA--DMDKDI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILTTFQKTFKGLLPLIILVAYTLLGAWIFWMIEGENE---k, MLTEQQK------
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87; Conservative
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; 82/2; 101/3; 157/1; 197/1; 230/ii
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25.4%;
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                                                                                                                                                                                                                                                                 Score 263; DB 2;
Pred. No. 1.2e-13;
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Pred. No. 2.6; 4:
3; Mismatches : 7;
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                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB/EMBL/DCL
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                                                                                                                                                                                                                                                   124; Indels
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                                                                                                                                                                                                                                                                                 Length 452
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                                                                                                                                                                                                                                                                                                                                     325/3;
               -SALDAIYFV
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                                                                                                                                                                                                                                                                                                                                     356/1; 404/3
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RESULT 14
T30037
hypothetical protein F20Al.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30037
R;Gattung, S; Wu, X
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F20Al.
A;Reference number: Z20726
A;Accession: T30037
**Cfratus: preliminary: franslated from GB/EMBL/DDBJ
**Cfratus: preliminary: franslated from GB/EMBL/DDBJ
hypothetical protein W06D12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26229 R;Basham, V.
                                                                                                                         RESULT
T26229
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A:Map position: 5
A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110
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A;Molecule type: DNA
A;Residues: 1-1539 <GAT>
A;Cross-references: EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1.
A;Experimental source: strain Bristol N2; clone F20A1
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A;Gene: CESP:W06D12.2
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A;Accession: T26229
A;Status: preliminary; translated from GB/EMBL/DD;J
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A; Residues: 1-444 <WIL>
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POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD
CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHAN
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DOMAIN
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                      CHANNEL SUBUNIT).
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                                                                                          CIW2_HUMAN
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                                                                                                                                          361
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                                                                                                                                         MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLII 60
                                                                                                                                                                              AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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                                                                                                                                                                                                                                                             LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
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              OR TREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channel;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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REQUIRED FOR BASAL CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
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                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usige by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE, POTEIN (POTENTIAL),
-i- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH-
CHLOROFORM, HALOTHANE AND ISOFLURANE
-i- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN NAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Price L.A., Hellings S.E., Hayashi J.H., Pan. Th. M.H.; Submitted (MAY-1997) to the EMBL/GenBank/DDF.d databases -i- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Price L.A., Hellings
Submitted (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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603219; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurosci. 2:422-426(1999).
                                                                           391;
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long
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95.1%;
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N-LINKED (GLCNA)
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A -> T (IN REF
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Pred.
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CYTOPLASMIC (F
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Catarrhini; Hemini
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                                                                           Mismatches
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No. 1.7e-14
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two-pore-domain
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ackground K+
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
                                                                                                                                                                                                                                                                                                                 Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S. "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
                                               use by non-profit instructions are modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sb.ch).
                                                                                                                This SWI
between
InterPro;
InterPro;
                                                                                                                                                                                                                                  Submitted (MAR-2000) to the
                                                                                                                                                                                                                                               chromosome 11."
                                                                                                                                                                                                                                                                       Gray A.T.;
                                                                                                                                                                                                                                                                                 TISSUE=Frontal cortex;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                             PubMed=11042359;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                       EMBL;
                                                                                                                                                                                                                                                       *Assignment of KCNK4 encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
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                                                                                                  s SWISS-PROT entry is copyright. It is produced throughen the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no re
                                                                                                                                                           FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARD POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTE SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF
                                                                                                                                                   CHANNELS
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                      AF248242;
AF247042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
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IPR001622;
IPR003280;
                                                                                                                                                                                                                                                                                           N.A.
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                      AAG31731.1;
AAF64062.1;
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Primates;
                      ALT_INIT.
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Catarrhini; Hominidae;
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PRINTS; PR01333; 2POREKCHANEL.
Ionic channel; Transmembrane; Ion transport; Potassium transport;
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SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND ALTERNATIVE SPELICING.
2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE.
TISSUE SPECIFICITY: DEPRESSED IN BRAIN, SPINAL CORD AND EYE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROFORM, DIETHYL SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
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LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA
                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
                               LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
                                                                                     CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI
                                                                                                                                         CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
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                                                                  CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQNSPAYQPLVWFWI
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N-LINKED (GLCNAC. ...) (POTENTIAL).
KLLVE -> KAMAI (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
478A834B7B7AEC92 CRC64;
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Pred. No. 8e-
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01-0CT-2000 (Rel.
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-!- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITI...
POTASSIUM CHANNEL. OUTWARD RECTIFICATION :.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACID - CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-SAKKONK5 OR TASK2.
                                                                                                     SEQUENCE
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                 Ionic channel; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF084830; AAC79458.1; MIM; 603493; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
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Lazdunski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is proxibetween the Swiss Institute of Bioinforma "\sims
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       channel from human kidney.
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Reyes R., Duprat F., Lesage F., Fink M., Salin s M.,
                                                                                                                         CARBOHYD
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SIMILARITY: BELONGS TO THE TWO PORE DOMAIN.
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SUBUNIT: HOMODIMER (POTENTIAL).
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                       20.1%;
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POTENTIAL. 5.
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ALSO DETECTED
THE KIDNEY, EXPRESSION
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000180; Q13307;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFANILY K MEMBER 1 (INWARD RECTIFYING CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL KCNO1).
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                                                                                                                                                                                                                                                                                                                  Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.; "Sequence and function of the two P domain potassium implications of an emerging superfamily."; J. Mol. Med. 76:13-20(1998).
                                                                                                                                                                                                                                                          Desir G.V., Orias M.,
Submitted (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel structure.";
EMBO J. 15:1004-1011(1996)
                   This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on if
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barhanin J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96183184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE~Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCNK1 OR TWIK1 OR HOHO1
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98122696; PubMed=9462864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "TWIK-1, a ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lesage
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                                                                                                          IT G.V., Orias M., Freeman T.;

mitted (APR-1997) to the EMBLY-GenBank/DDBJ databases.

mitted (APR-1997) to the EMBLY-GenBank/DDBJ databases.

MICCTION: MEAKLY IWWARD RECTIFYING POTASSIUM CHANNEL.

SUBCUIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INVEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN KIDNEY.

MISCELLANDOUS: INHIBITED BY BARIUM, QUININE, QUINIDLE AND

INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
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mare E., Fink M.
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                                        a collaboration
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or send a
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 TISSUE=Brain;
                                                                                                             Mus musculus
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                     SEQUENCE FROM
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01-OCT-2000 (Rel. 4
POTASSIUM CHANNEL S
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EMBL; U76996; AAB97878.1;
EMBL; U90065; AAB51147.1;
MIM; 601745; -.
                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02034; TWIK_channel; 1.
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InterPro; IPR001779;
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                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                STANDARD;
                                                                                                 TWIK-1).
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40, Last sequence update)
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5UBFAMILY K MEMBER 1 (INN)
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                                           Chordata;
Rodentia;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTE
T->A: NO EFFECT ': CHANNEL A

M; 2A41D95013232150 CRC64;
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CYTOPLASMIC
POTENTIAL.
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Pred. No. 5.
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                                        Craniata; Vert*: ita; |
Sciurognathi; Y: dae;
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Mismatches '9;
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                                                         Euteleostomi;
                                            Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transport;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arrighi I., Lesage F., Scimeca J.-C., "Structure, chromosome localization, a mouse twik K+ channel gene."; FEBS Lett. 425:310-316(1998).
                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                   PRINTS; PR01096; TWIK1CHANNEL. PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                       InterPro; IPR001622; -.
InterPro; IPR001779; -.
InterPro; IPR003280; -.
                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF033017; AAC16973.1; MGD; MGI:109322; Kcnkl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurte: Lazdunski M.;
"The structure, function and distribution of the mouse TWIK-1
                                                                                                                              CARBOHYD
                                                                                                                                         DOMAIN
                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                           Glycoprotein
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                                                                                                                                                                                                                                                                                                             Pfam; PF02034; TWIK_channel; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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Lesage F., Lauritzen I., Duprat F.,
                        51
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIA
TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION I
KINNEY, THYROID, SALLVARY GLAND, ADREMAL CLAND, PROSTATE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: INHIBITED BY QUININE, ACIDIFICATION. ACTIVATED BY PROTEIN I SIMILARITY: BELONGS TO THE TWO PORE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONCEPTION. EXPRESSIC STABILIZES AFTER DAY
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                  FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT
FLVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE 84
                                                   103;
                                                                                                                                                                                                                                                                        channel;
                                                             Similarity
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28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSION DETECTED AS EARLY AS
ON INCREASES FROM 2-8 DAYS AFTER
                                                                                                                M.
                                               72;
                                                Score 370; DB
Pred. No. 1.5e
72; Mismatches
                                                                                                               N-LINKED (GLCNAC. . .) (I
A996060A18266FD4 CRC64;
                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                        PORE-FORMING POTENTIAL.
                                                                                                                                                                  POTENTIAL.
PORE-FORMING
                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                       Ion transport; Potassium
                                                            370;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N KINASE
DOMAIN
                                                            DB 1;
.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BARIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIGHEST EXPRESION IN BRAIN,
                                                                                                                                                                                                                    (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.
FAMILY
                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND INTERNAL
                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFTER BIRTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                      transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 DAYS POST
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                                                                                                                                                                                                                                                                                                                                                                                                                                          for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
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                                                Gaps
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EMBL; AF006823; AAC51777.1;

1.64

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p://www.isb-sib

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restrictions EMBL is

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collaboration -

outstation

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RESULT 8
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014649;
01-0CT-2000
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
                                                            -
                                                                                                                                          + +
                                                                                                                                                                                                                                                                                                                                                                 MEDILNE-99254548; PubMed=10321245; MEDILNE-99254548; PubMed=10321245; Ri. M., Ri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
MEDLINE=97459932; PubMed=9312005;
Fink M., Reyes
                                                                                                                                                                                                                                                                                                                          channels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCNK3 OR TASK.
                     -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                   "Inhalational anesthetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "TASK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85
                                    FUNCTION: PH-DEFENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN, RECTIFICATION DIRECTION RESOURS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MESBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS INWARD. SUBCELLULAR LOCATION: INTEGRAL MESBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN, LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON. MISCELLANBOUS: INHIBITED BY EXTERNAL ACTIVATED BY HALOTHANE AND ISOFLURANE.
CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  physiological pH.";
J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGN, RTEGGKIFCIIYALLGIP
                                                                                                                                                                                                                                                                                                       Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVKRKLSAELAG -- NHNQELTPCRRTLSVNHLTSEREVLPP' LKAES - IYLNGLTPH 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a human background K+ channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human).
                                                                                                                                                                                                                                                                                                          2:422-426(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                     BELONGS TO THE TWO PORE DOMA IN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ETFCELHELK - -
                                                                                                                                                                                                                                                                                                                                              activate two-pore-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertel rata;
Catarrhini; How Wildae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Heurteaux C., Lazdunski M.; sense external pH variations
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                                                                                                                                                                                                                                                                                                                                                y G., Lazdunski
ain background
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ackground K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KFRKMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                          CIMI_MOUSE STANDARM;

O35111; O35163;

O1-OCT-2000 (Rel. 40, Created)

O1-OCT-2000 (Rel. 40, Last sequence update)

O1-OCT-2000 (Rel. 40, Last annotation update)

O1-OCT-2000 (Rel. 40, Last annotation sequence)

POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL POTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K-CHANNEL)

CHANNEL POTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K-CHANNEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionic channel; Transmembrane;
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01095; TASKCHANNEL PRINTS; PR01333; 2POREKCHANEI
                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003092;
InterPro; IPR003280;
SEQUENCE
                               Mammalia; Eutheria;
                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000099; InterPro; IPR001622;
                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                 QRATSVKRKLSAELAGNHNQELTPCRRTL 369
| | | : | : | | | | | | | |
TSDTCVEQSHSSPGGGGRYSD-TPSRRCL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                      GEFRAHAAEWTA-----
                                                                                                                                                                                                                                                                                                          QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRDAEHRALLTRNGQAGGGG
                                                                                                                                                                                                                                                                                                                      ELERVVLRL-KPHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELDELIQOIVAAINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI
                                                                                                                                                                                                                                                              GGGSAHTTDTASSTAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLS
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FROM N.A
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244
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                                                      (Mouse)
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101
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                               Chordata;
Rodentia;
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28.08;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                      NVTAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 370;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (P
9FF4C8266F615FB7 CRC64;
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                                           Craniata;
                               Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transport;
                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; L
1.8e-18;
hes 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                            ---FKETRRRLSVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                 Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                               Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                    MSV---
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                               Mus
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EMBL; AB008537; EMBL; AF006824; EMBL; AB013345; EMBL; AF241798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20287574; PubMed=10748056; Lopes C.M., Gallagher P.G., Buck M.E., Butle & H., Golds "Proton block and voltage gating are potassi", lependent cardiac leak channel konks.";
J. Biol. Chem 275.1600.
                                           CONFLICT
CONFLICT
SEQUENCE
                                                                                DOMAIN
CARBOHYD
                                                                                                         DOMAIN
TRANSMEM
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See lange://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97459932; PubMed-9312005;
Duprat F., Lesage F., Fink M., Reyes
"TASK, a human background K+ channel
near physiological pH.";
EMBO J. 16:5464-5471(1997).
                                                                                                                                                                                                                      PRINTS; PRO1095; TASKCHANNEL. PRINTS; PRO1333; 2POREKCHANEL. Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98165556; PubMed=9506712; Kim D., Fujita A., Horio Y., Kurachi Nationing and functional expression of background K+ channel (cTBAK-1)."; Circ. Res. 82:513-518(1998).
                                                                                                                                                                                                                                                                                                 InterPro; IPR000099; -. InterPro; IPR001622; -.
                                                                                                                                                                                                                                                                                                                            EMBL; AF242508; AAF81418.1; MGD; MGI:1100509; Kcnk3.
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                                                                                                                                                                                                              Glycoprotein
                                                                                                                                                                                                                                                            Pfam; PF02034; TWIK_channel; 1.
                                                                                                                                                                                                                                                                        InterPro; IPR003092; -
InterPro; IPR003280; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOL. CHEM. 275:1659-16978 (2000).

BIOL. CHEM. 275:1659-16978 (2000).

FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSIT, I, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION, SULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE CONCENTRATION ON EXTERNAL POTASSITY ONCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION I
                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE. FISIN (POTENTIAL).

TISSUE SPECIFICITY: VERY STRONG EXPRESS: IN HEART, ALSO DETECTISSUE SPECIFICITY. SKIN, TESTIS, LUNG, SKILETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN MISCELLANEOUS: INACTIVATED BY BARIUM.

MISCELLANEOUS: INACTIVATED BY BARIUM. MISCELLANEOUS: INACTIVATED BY BARIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHANNELS.
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108
108
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223
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; AAC53367.1;
; BAA28349.1;
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101
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53
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                                                      PORE-FORMING (POTINTIAL).

POTENTIAL.

CYTOPLASMIC (POTE::IIAL).

N-LINKED (GLCNAC...) (PC
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PORE-FORMING
POTENTIAL.
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POTENTIAL.
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Score

Length 409;

InterPro; InterPro;

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RESULT 1
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Best Local
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O1-OCT-2000 (Rel. 40, Created)
O1-OCT-2000 (Rel. 40, Last sequence update)
O1-OCT-2000 (Rel. 40, Last annotation update)
O1-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE FOTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE FOTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE K+ C
                                     use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           Leonoudakis D., Gray A.T., Winegar B.D., Kindler C. Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S. "An open rectifier potassium channel with two pore
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98099797; PubMed-9437008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIW3_RAT
                                                                                                                                                                                                                                                                                                                                                                cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                         oned from rat cerebellum.";

Neurosci. 18:868-877(1998);

NEURCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
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                                                                                                                                                      BUPIVACAINE A SIMILARITY: I CHANNELS.
                                                                                             s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                                                          (BY SIMILARITY).

(BY SIMILARITY).

SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE

EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AN
                                                                                                                                                                                            MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC,
                                                                                                                                                                                                                                                                               WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTQPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMANMVLIGFVSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIISTIIFILFGCVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSD--I
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              AF031384;
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             AAC39952.1;
                                                                                                                                                                                 AND PHENYTOIN.
                                                                                                                                                                    BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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31.1%;
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Sciurognathi;
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RESULT 11
CIWG_HUMAN STANDARD; PRT: 313 AA
ID CIWG_HUMAN STANDARD; PRT: 313 AA
ID CY257;
AC 09Y257;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 6 (INN.) RECTIFYING
DE CHANNEL PROTEIN TWIK-2) (TWIK-ORIGINATED SINGLARITY SEQUEN
GN KCNK6 OR TWIK2 OR TOSS.
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Best Local
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                                      Pountney D.J., Gulkarov I., Vega-Saenz de M. Saganich M., Rudy B., Artman M., Coetzee W., "Identification and cloning of TWIK-origina-(TOSS): a novel human 2-pore K+ channel pri: S. FEBS Lett. 450:191-196/1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
SEQUENCE
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DOMAIN
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PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01333; 2POREKCHANEL.
    TISSUE=Brain;
MEDLINE=99175162;
                     SEQUENCE FROM N.A.,
                                                                                                                                       Eukaryota;
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                           TISSUE=Testis
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                         QTQPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMN
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                                                                                                                              Eutheria;
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                     AND
                                                                                                                               Chordata;
Primates;
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31.1%;
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                     MUTAGENESIS
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Pred.
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: D2778016E09E2H 5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (P. W. TIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                               Craniata; Ver'
Catarrhini; H
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                                                                                                                                                                                                                                                                                                   LTTIGFGDYVALQKDQAL
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                                                        similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :NTIAL)
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                                                subunit
                                                                          Holmes
                                                                                                                                       Euteleostomi;
                                                                                                                                                                  SEQUENCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport;
                                                  sequence
                                                                                                                                                                          POTASSIUM
                                                                                                                                                                                                                                                                 267
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Query Match
Best Local S
Matches 83
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MUTAGEN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            potassium channel family.";
J. Biol. Chem. 274:7887-7892(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM -!- SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chavez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J., Mehta Y., Forsayeth J.R., Yost C.S.; Mehta Y., Forsayeth J.R., Yost C.S.; "TWIK-2, a new weak inward rectifying member of the tandem pore domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ionic channel;
                                                                                                                   173
                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                            Local Similarity
nes 83; Conserv
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TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED
IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOWEST EXPRESSION DETECTED IN BRAIN.
MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHANNELS
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                      KHI-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAV
                                                                                                                                                                            LGNSSNQVS----HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF
                                                                                                                                                                                                                                                                        YLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIP 116
                                                                                                                 LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVA--LPAVIF
                                                                                                                                                        LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTML 136
                                                                                                                                                                                                                                 YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVV 76
AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAMVLV
                                                                             LLTASAQRLSLL----LTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIF
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Forsayeth J.R., Yost C.S.;
Chem. 274:24440-24440(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD22980.1; -. AAD24000.1; -.
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                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                 Score 342; DB 1;
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
C->A: NO CHANNEL ACTIVITY.
1379382DFB0575DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
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PORE-FORMING
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PORE-FORMING
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                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          There are no restrictions on ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                              104;
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           RA Dodson K., Doup L.E., Downes M., Dugan-Rocha J. Dunn P.,
RA Durbin K.J. Evangelista C.C., Ferraz C., Ferraz C., Ferraz S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan F., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei R., H., Ilbeywam C.,
RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.F., Ncherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Mory S. J., Moshrefi A.,
RA Mender G., Kalush F., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Sradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wully S., Yao Q.A.,
RA Yellams S.M., Woodage T., Worley K.C., Wully S., Yao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng R.A., Myers E.W., Rubin G.M., Venter T.C.,
The genome sequence of Drosophila melanogusier.";
RT The genome sequence of Drosophila melanogusier.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20196006; PubMed=10731132;

A Adams M.D., Celniker S.E., Holt R.A., Evans C..., Gocayne J.D.,

A Adams M.D., Celniker S.E., Li P.W., Hosk h R.A., Galle R.F.,

A Amanatides P.G., Scherer S.E., Li P.W., Hosk h R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Ashburn M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhawi Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhawi Q., Chen L.X.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhawi Q., Chen L.X.,

Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews J., McCh. C., Baldwin D.,

A Abril J.F., Agbayani A., An H.-J., Bayrakt J., Bolshakov S.,

Ballew R.M., Basu A., Baxendalle J., Bayrakt J., Bolshakov S.,

Beeson K.Y., Benos P.V., Berman B.P., Bhand J., Bolshakov S.,

Beeson K.Y., Benos P.V., Bouck J., Brotkier P.,

A Berkova D., Botchan M.R., Bouck J., Brotkier P.,

A Borkova D., Botchan M.R., Bouck J., Brotkier P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport J. 3, Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Davenport J., Bott S.M.,

Bodcon K. D., Botcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,

Bodcon K. D., Botcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,

Bodcon K. D., Botcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
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Q94526;
Q1-OCT-2000
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Pterygota; Ne
Ephydroidea;
Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein S.A.N., Price L.A., Rosenthal D.N.. \chi ausch M.H.; "ORK1, a potassium-selective leak channel with a potassium open domains cloned from Drosophila melanogaster by expression in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHANNEL ORK1).
ORK1 OR CG1615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerevisiae."
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POTASSIUM CHANNEL.
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  RECTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insecta;
  SI
                                                                                        Zheng L.,
Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Χ.A.,
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RESULT 13
CIW8_MOUSE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003484; AAF47972.1; -. FlyBase; FBgn0017561; Ork1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U55321; AAC69250.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                      299 VGYLRRMLN-ELY 310
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SUBCELLULAR LOCATION: INTEGRAL
TISSUE SPECIFICITY: WIDESPREAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHANNELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: INHIBITED BY BARIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXPRESSION IN MUSCLE, BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN LARVA AND EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                 GIPVNGILFAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFLVVVLYLIIGAAVFKALEQPQE----ISQRTTIVIQKQTFIAQHACVNSTELDELIQQ 105
                                                                                                       FKETRRRLSVEIY
                                                                                                                                         FV--IVWF--IFSLGYLVMIMTFITRGLQ--SKKLAYLEQQLSSNLKATQNRIWSGVTKD
                                                                                                                                                                        FYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKK----TKEEVGEFRAHAAEWTANVTAE
                                                                                                                                                                                                           IALFLLLPSWVFTYFENWPYSISLYYSYVTTTTIGFGDYVPTFGANQPKEFGGWFVVYQI
                                                                                                                                                                                                                                           CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVA------GGSDIEYLD
                                                                                                                                                                                                                                                                                                                  GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-----QTKIRIISTIIFILF-G
                                                                                                                                                                                                                                                                                                                                                     ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI
                                                                                                                                                                                                                                                                                                                                                                                     IVAAINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
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Pred.
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W; 09AE1A3669072E07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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POTENTIAL.
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PORE-FORMING
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EAD EXPRESSION IN ADULT, STRONGEST
AND OVARY. ALSO PRESENT AT LOW LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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No. 5.7e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transport;
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"Cloning of a tesis.";
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0922T1; 097242; 0971V1; 0902Y8; 090XY0;

01-OCT-2000 (Rel. 40, Created)

01-OCT-2000 (Rel. 40, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)
                                                     EMBL;
                                                                                                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gan L., Joiner W.J., Quinn A.M.,
Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bockenhauer D., Nimmakayalu
Gallagher P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain, and MEDLINE=99223496;
                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2-307 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1998) to the EMBL/GenBank/DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 15-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of a new mouse two-P domain channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opes C.M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (POTENTIAL).

SUBUNIT: HOMODIMER (POTENTIAL).

TISSUE SPECIFICITY: DETECTED IN EMBRYO.

WEAKLY EXPRESSED IN COLON, TESTIS, ATLANTY GLAND, THE STEM, BLADDER, UTERUS, OVARY, SALIVARY GLAND, THE STEM, DETECTED IN BRAIN, CEREBELLUM, SPINAL COLOR HOLDER, VENTRICLE, SKELETAL MUSCLE, LIVER, PLACENTA AND PANEY AS IN THE EYE, HIGH EXPRESSED IN THE RETINAL GANGLION CELL LAND INNER NUCLEAR
                                                                                                                                                                                                                                                                                                                                   LAYER.
SIMILARITY: BELONGS
CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REACH THE PLASMA MEMBRANE
                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
                       AF110521;
AB015729;
                                                                                                        non-profit institutions as long
and this statement is not removed
requires a license agreement (See
an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 localization, channel KCNK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JUN-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with
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new double-pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buck M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a unique pore structure.";
274:11751-11760(1999).
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BAA35074.1;
AAD09337.1;
                                                        AAD29577.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lung;
PubMed=10206991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goldstein S.A.N.;
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                                                     ALT_TERM
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channel
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                                                                                                                                                                                                                                                           It is produced through a conformation and the EMBL
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chi; Suridae;
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                                                                                                                                                           as is content is in the injury of the injury
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Murinae; Mus
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DOMAIN
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Lazdunski M.;
"Cloning of a nu
homologue with
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CARBOHYD
                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003280;
                                                       SEQUENCE FROM N.A.
                                      MEDLINE-99223496;
                                                TISSUE-Brain;
                                                                                                                          POTASSIUM CHANNEL
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                                                                                                                                                                                                                                                                                                                                    LGAVLRAQAHGVSSLGNGS-ETSNWDLPSALLFTASILTTTGYGHMAPLSSGGKAFCVVY
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Similarity 29.6%;
84; Conservative (
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AAF14528.1;
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                                      PubMed=10206991;
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Primates;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

NGS -> TR (IN REF. 4).

GS -> TR (IN REF. 4).

GS -> THSREFGPRGEEFGTR (IN REF. 2).

GS -> GS -> THSREFGPRGEEFGTR (IN REF. 2).

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MW; 567D32AE335BA44F CRC64;
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Pred. No. 3.5e-14;
5; Mismatches 94;
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CYTOPLASMIC ()
POTENTIAL.
PORE-FORMING
 structure
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                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
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         domain channel
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lon_update)
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         subunit and
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EMBL; AF11052
MIM; 603940;
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SEQUENCE
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                             183
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  237
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                                                                                                                                     67
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FUNCTION: PROBABLE POTASSLUM CHANNEL
OBSERVED IN VITRO AS PROTEIN REMAINS
MAY NEED TO ASSOCIATE WITH AN AS YET
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SUBCELLULAR LOCATION: INTEGRAL MEMBR
SUBCELLULAR LOCATION: INTEGRAL MEMBR
ALTERNATIVE PRODUCTS: 3 ISOFOMS; A
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TWO PORE
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ALLGYLLLGL---
                                                                 VALPAVIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWF----
                                                                                                               ALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNV5.)TKIRIISTIIFILFGCVLF
                                                                                                                                                                               WSRYGLLVVAHLLALGLGAVVFQALEGPPACRLQAELRAEI
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AF110523;
                    ----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFR/ HAAEW--TANVTAE 324
                                                                                         AALGLPASLALVATLRHCLLPVLSRPRAWVA----VHWQLSPARAALLQAVALGLLVASSF
                                                                                                                                     LGTALATQAHGVSTLGNSS-EGRTWDLPSALLFAASILT [1]
                                             VLLPALVLWGLQGDCSLLGAVYFCFSSLSTIGLEDLLPG
                                                                                                                                                 AF110522;
                                                                                                                                                                                                                              Similarity
88; Conserv
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307
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241
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 LAML-----LAVETFSELPQVRAMGKFFRPSGPVTAE
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                                                                                                                                                                                                                            Score 300.5; DB Pred. No. 7.6e-1:60; Mismatches .!
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POTENTIAL.
CYTOPLASMIC (POTITIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                        (GLCNAC...) (POTENTIAL)
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RESULT 15

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TRANSMEM CONFLICT
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PIR;
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EMBL;
EMBL;
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P40310; Q05721;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
0UTWARD.RECTIFIER POTASSIUM CHANNEL TOKI (TWO-DOMAIN OUTWARD RECTIFIER
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: OUTWARDLY RECTIFYING POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miosga T., Witzel A., Zimmermann F.K.;
"Sequence and function analysis of a 9.46 kb
Saccharomyces cerevisiae chromosome X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K+ CHANNEL YORK).
TOK1 OR DUK1 OR YJL093C OR J0911
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                         "The S. cerevisiae outwardly-rectifying potassium channel identifies a new family of channels with duplicated pore Recept. Channels 4:51-62(1996).
                                                                                  TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                            Romey G.,
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guy H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reid J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96303826; PubMed=8723646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 376:690-695(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A new family of outwardly rectifying potassium channel proteins with two pore domains in tandem.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldstein S.A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95379951; PubMed=7651518;
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                                                                                                                   Conic channel
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; U28005; AAC49070.1;
; U39403; CAA64176.1;
; U37254; AAC49168.1;
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$47058; $47058.
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Ogeru5 rattus norv
Ogj1d4 rattus norv
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Oges08 rattus norv
Ogjj14 mus musculu
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Q9hb59 homo sapien
Q9hb59 homo sapien
Q9h591 homo sapien
Q9jk62 mus musculu
Q9z2t2 rattus norv
Q022t2 roryctolagus
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Q9hbc8 homo sapien
Q9j158 cavia porce
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076795 caenorhabdi
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ALIGNMENTS

Oy Db Oy	Qy Db	z wo	Q9NRT2 AC OCC OCC OCC OCC OCC OCC OCC OCC OCC O	RESULT
61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120	1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAIN (NKTVSTIFLVVVLYLII 60 	Query Match 97.8%; Score 2044; DB A. Length 411; Best Local Similarity 96.4%; Pred. No. 3.1e-1;; Matches 396; Conservative 11; Mismatches 1; Indels 0; Gaps 0;	OPNRT2 OPNRT2 OPNRT2 OPNRT2 OPNRT2 O1-OCT-2000 (TrEMBLrel. 15, Created) O1-OCT-2000 (TrEMBLrel. 15, Last sequence on date) O1-OCT-2000 (TrEMBLrel. 16, Last sequence on date) O1-MAR-2001 (TrEMBLrel. 16, Last sequence on date) O2-MAR-2001 (TrEMBLRel. 16, Last sequence on date) O3-MAR-2001 (TrEMBLRel. 16, Last sequence on date) O4-MAR-2001 (TrEMBLRel. 16, Last sequence on date) O5-MAR-2001 (TrEMBLRel. 17, Last sequence on date) O5-MAR-2001 (TrEMBLRel. 17, Last sequence on date) O5-MAR-2001 (TrEMBLRel. 17, Last sequence on date) O5-MAR-2001 (TrEMBLRel. 18, Last sequence on date) O6-MAR-2001 (TrEMBLRel. 18, Last sequence on date) O7-MAR-2001 (TrEMBLRel. 18, Last sequence on date) O7-MAR-2001 (TrEMBLRel. 18, Last sequence on date) O8-MAR-2001 (TrEMBLRel. 18, Last sequence on date) O8-MAR-2001 (TrEMBLRel. 18, Last sequence on date) O9-MAR-2001 (TrEMBLRel. 18, Last seq	OLT 1

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MEDLINE=20298807; PubMed=10747911;
Bang H., Kim Y., Kim D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JIS4;
01-OCT-2000
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InterPro; IPR00380; -.
Pfam; PF02034; TMIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
SEQUENCE 538 AA; 59800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family.";
J. Biol. Chem. 275:17412-17419(2000)
EMBL; AF196965; AAF75132.1; -.
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01-MAR-2001
01-MAR-2001
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Last sequence updaya)
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Q9HB59 PRELIMINARY;
Q9HB59;
Q1-MAR-2001 (TrEMBLrel. 16, 0
Q1-MAR-2001 (TrEMBLrel. 16, 1
Q1-MAR-2001 (TrEMBLrel. 16, 1
QP DOMAIN POTASSIUM CHANNEL T
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Ionic channel.
SEQUENCE 538 AA; 59764 MV
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SEQUENCE FROM N.A.

MEDLINE=20435789; PubMed=10880510;
Lesage F., Terrenoire C., Romey G., Lazdunski ...

"Human TREK2, a 2P domain mechano-sensitive K.: hannel with multiple regulations by polyunsaturated fatty acids, 1. phospholipids and Gs, Gi, and Gq protein-coupled receptors.";

J. Biol. Chem. 275:28398-28405(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertek ıta; i
Mammalia; Eutheria; Primates; Catarrhini; Homi.idae;
                                                                                                                                                                                                                    NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISF: 3GKIFCIIYALLGIPLF 170
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                                                                                                                  -KRKLSAELAGNHNQELTPCRRTL
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                                                                                  ERRRLGLDQRAHSLDMLSPEKRSV
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Pred. No. 2.5e
54; Mismatches
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                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-129/SVJ; TIS ROUX J., Barhanin J "Mouse two P domain
                                                                                                                                                                                                                               Dl. Par.
POTASSIUM CHARRED
Mus musculus (Mouse).
Metazoa; Chordata;
Theria; Rodentia;
                                                        Cid L.P., Niemeyer M.I., Sepulveda F.V.;
"Functional properties of mouse TASK-2 potassi
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; AF259395; AAF68668.1; -.
EMBL; AF319542; AAG35065.1; -.
                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update
POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
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Mammalia; Eutheria;
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DJ137F1.2 (1
  SEQUENCE
                                                                                                                     TISSUE-KIDNEY;
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                        Submitted (APR-2000)
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InterPro; IPR003280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPLNVIFL----NHLGTGLRAHLAAIE----RWEDRPRRSQVLQVLGLALFLTLGTLVIL
            channel
                      PR01333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
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  502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                 hanin J.;
domain potassium
 Ā
                                                                                                                                                                                          TISSUE-KIDNEY;
                         2POREKCHANEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
 55976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32507 MW;
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OF 7
                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
THE POTASSIUM CHANNEL SUBFAMILY K).
                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 499.5;
Pred. No. 7.
                                                                                                                                                                   channel TASK2.";
                                                                                                                                                                                                                                         Craniata; Vertebrata; i
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCBA3B352F1F0952 CRC64;
E4C7E7CC71B44D95 CRC64;
                                                                                                                                                                                                                                                                                                                                          502
                                                                                             potassium channel.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3e-29
                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                         update)
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                                                                                 databases.
                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                          Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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Best Local S
Matches 99
                                                                                               Matches
                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999
01-MAY-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9Z2T2
Q9Z2T2;
                                                                                                                                                                                                                      Submitted (SEP-1997) to the EMBL; AF022819; AAD09336.1; InterPro; IPR000099; -. InterPro; IPR001622; -. InterPro; IPR001779; -.
                                                                                                                                                                      InterPro; IPR003280;
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01096; TWIK1CHANNEL.
                                                                                                                                                       Ionic channel. SEQUENCE 336
                                                                                                                                                                                                                                                                                "Cloning and localization two P domains.";
                                                                                                                                                                                                                                                                                                                                                          викагуота; Metazoa; Chordata; Craniata; Vertel "ta; I
Mammalia; Eutheria; Rodentia; Sciurognathi; М. idae;
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                PUTATIVE POTASSIUM CHANNEL
                                                                                                                                                                                                                                                                                                        Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                 Gan L., Joiner W.J.,
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
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                             109
                                                                                                      Local
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         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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                                                               FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTI'IAQJIACVNSTELDELIQQIVA 108
                   AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGH!SPRTEGGKIFCIIYALLGIP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMAGS----TASKDVNIFSFLSKKEETYNDLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETREE. F.EIYDKFQRATSVKRKLSA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIST1.F1LFGCVLFVALPAVIFKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYC
                                                   FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALY6) = ELWIYLGLAW----LSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTWI-SALGKFFGGRAKRLGQFLTRRGVSLRKAQITCTA IVWGVLVHLVIPPFVFMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAITGNQT--FNNWNWPNAMIFAATVITTIGYGNVAPKI, AGRLFCVFYGLFGVPL---C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEF!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     (TremBLrel. 10, Created)
(TremBLrel. 10, Last sequence upar (TremBLrel. 16, Last annotation up
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                       AA;
                                                                                                                                                       38228 MW;
                                                                                                        18.0%;
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                                                                                                                                                                                                                                                                                                                  Quinn A.M.,
                                                                                                                                                                                                                                                                                           of
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                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                  TWIK.
                                                                                                                                                                                                                                                                    EMBL/GenBank/DDF
                                                                                              Score 375.5; DB H Pred. No. 9.4e-20; 2; Mismatches 10H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 409;
Pred. No. 5.
                                                                                                                                                                                                                                                                                           rTWIK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VEVHKAIKKRRRFFE
                                                                                                                                                       5E78031947D750E6
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                                                                                                                                                                                                                                                                                                             L. -Y., **
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LSDGGKAFCIIYSVIGIP
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                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                Murinae;
                                                                                                                                                                                                                                                                                            channel
                                                                                               17;
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                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277
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न्द्र केल्स्स्ट्रिक हो। अक्टूबर्ग

17

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RESULT
Q9HBC8
AC Q9
DT Q1
DT Q1
DT Q1
DT Q1
OT Q1
OT Q2
OT Q1
OT Q2
OT Q1
OT Q2
OT Q1
OT Q2
OT Q1
OT Q1
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002821
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 78
                                       Q9HBC8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TWO PORE POTASSIIM CHANNEL KT3.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence u
01-MAR-2001 (TrEMBLrel. 16, Last annotation
DOUBLE PORE POTASSIUM CHANNEL RABKCNK1 (FR/
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
PRINTS; PR
PRINTS; PR
               Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; [
                                                                                                                          09нвс8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orias M., Velazquez H., Tung
Submitted (MAY-1997) to the E
EMBL; AF004695; AAB61602.1;
InterPro; IPR001622; -
  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  002821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001779; -.
InterPro; IPR003280; -.
InterPro; IPR003280; -.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01096; TWIK1CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                51 FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                         AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIME 295
                                                                                                                                                                                                                                              FTLLFLTAVVQRVTVHVTR---RPVLYFHVRWGFSKQVVAIVHAVLLGLITVSCFFFIPAA
                                                                                                                                                                                                                                                                         LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTLLELTAVVQRVTVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFI--P
                                                                                                                                                                                                                                                                                                     ANNYGVSVRSNASGN-WNWDFASALFFASTVLSTTGYGHTVPLSDVGKAFCIIYSVIGIP
                                                                                                                                                                                                                                                                                                                                                         FLVLGYLLYLVFGAVVFSSVELPYEDILLRQELRKLKRRFVEEHECLSEQQLEQFLGRVLE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAAVLSMIGDWLRVISK-----KTKEEVGEFRAHAAE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTII--FILFGCVLFVALP
                                                                                                                                                                                                                                                                                                                                                                                                                78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
29311 MW;
           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             16.9%;
33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                57;
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Last annotation update)
REL RABKCNK1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g F., Desir G.V.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                             Score 353.5;
Pred. No. 2.7e
57; Mismatches
                                                                                                                          PRT;
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94;
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                      O9JL58; PRELIMINARY;
09JL58; O1-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
                                                                    extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
EMBL; AF7212827; AAF63706.1; -.
InterPro; IPR000099; -.
InterPro; IPR001622; -.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
SEQUENCE 365 AA; 40769 MW;
                                   Pfam; PF02034; TWIK_channel; 1.
                                                                                                                                            Rajan S., Wischmeyer
Karschin A., Derst C.
                                                                                                                                                        MEDLINE=20287530; PubMed=10747866; Raian S., Wischmeyer E., Liu G.X.,
                                                                                                                                                                                     TISSUE=BRAIN;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                POTASSIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2000) to the EMBL; AF257081; AAG33127.1; Ionic channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Vega-Saenz de Miera E.C., Lau D.H.P.,
Coetzee W., Rudy B.;

"KT3.2 and KT3.3 Two Novel Human Two
                                               InterPro;
                                                          InterPro;
                                                                                                              "TASK-3, a novel tandem proe domain acid-sensextracellular histidine as pH sensor.";
J. Biol. Cham. 777 7777
                                                                                                                                                                                                                    NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                     KCNK9
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVLCTLCYLLVGAAVFDALESEAE - SGRQRLLVQKRGAJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFLVVVLXLIIGAAVFKALEQPQEISQRTTIVIQKQTF1 & ACVNSTELDELIQQIVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE -: -: NLVVAGLLACAATLALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTK:FILSTIIFILFGCVLFVALP
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                                              IPR003092;
IPR003280;
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                                                                                                                                                                                                                                 Rodentia;
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35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                    253
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                                                                                                                                                                                                                                                                                         Last sequence updat:)
Last annotation update)
                                                                                                                                                                                                                                                                                                                   Created)
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4; Mismatches
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Pred. No. 5.
                                                                                                                                                                                                                               Craniata; Verrebrata; Euteleostomi;
Hystricognathi; Caviidae; Cavia.
261DC973FF53AF91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA2A54D0615BC ;; CRC64;
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Query Match Best Local Similarity Matches 94; Conser

Conservative

59;

Score 351.5; Pred. No. 5.9e 59; Mismatches

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Gaps

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16.8%; 30.1%;

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RESULT
Q9QX34
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Best Loc
Matches
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SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
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Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gan L., Joiner W.J.,
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                                                                                                                       LIQQIVAAI---NAGIIPLGNSSNQVSHWDLGSSFFFFAGTVITTIGFGNISPRTEGGKIF 158
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CMFYALLGIPLTLVMFQSLGERI----
                                               CIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTK-----IRII
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299 AA;
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33325 MW; DCD41D8A212939C4 CRC64;
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                                                                                                                                                                                                                                                                                     ; Score 344; DB 11;
; Pred. No. 1.6e-17;
61; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α.Μ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                              QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVF
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Best Local
                                                                                                                                                                                                                                                                                      O76795 PRELIMINARY; PRT; 329 A.; O76795; O1-NOV-1998 (TrEMBLrel. 08, Created) O1-NOV-1998 (TrEMBLrel. 08, Last sequence to compare the compared of the compare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9H427 PRELIMINARY; PRT; 330 AA.
O9H427;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence of the colore)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation obtaine)
DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE Active CHANNEL PROTEIN TASK (KCNK3)).
SEQUENCE FROM N.A. Wang Z.-W., Salkoff L.; "Potassium channels in C. Submitted (AUG-1998) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2000) to the EMBL/GenBank/DDN: A. bases EMBL; AL118522; CAC14068.1; - SEQUENCE 330 AA; 36222 MW; 24F428721A1C7 CRC54;
                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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90; Conserv
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C. elegans.
the EMBL/G
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   EMBL/GenBank/DDe1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 343.5; DF
Pred. No. 2e-17:
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Ver or control (Catarrhini; Herist
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      databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · · NLVVAGLLACAATLALG
                                                                                                                                                                                                                                                                                                                                  ite)
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                                                                                                                                                                                                                                   Rhabditoidea;
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AF083652; AAC32863.1;

IPR000099;

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RESULT
Q9NPC2
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                                Q9NPC2;
Q9NPC2;
01-OCT-2000
                                                                                                                                                   | 21
SEQUENCE FROM N.A.
MEDLINE-20287530; PubMed-10747866;
Mischmeyer E., Liu G.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF08 InterPro;
                                                                                                                                                                                                   Girard C., Lesage F., T
"Human Task-3, a novel
Submitted (JUN-2000) to
                                                                                                                                                                                                                                                     KCNK9.
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; A
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InterPro;
                 SEQUENCE FROM N. TISSUE-BRAIN;
                                                                                                                  "TASK-3, a novel tandem proe domain acid-sensitive extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrembLrel. 15,
01-MAR-2001 (TrembLrel. 16,
2P DOMAIN POTASSIUM CHANNEL
POTASSIUM CHANNEL KT3.2) (2F
                                                                                      SEQUENCE FROM N.A.
Vega-Saenz de Miera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01333; 2POREKCHANEL. Ionic channel.
       PubMed=11042359;
                                              Submitted
                                                         6
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                          TASK1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                   and
                                                                   e W., Rudy
and KT3.3
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IPR003280;
                                              (APR-2000)
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1 2P domain potassium ch
to the EMBL/GenBank/DDBJ
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15,
                                                the
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16, Last annotation update)
NEL TASK-3 (POTASSIUM CHANNEL TASK3)
(2P DOMAIN POTASSIUM CHANNEL).
                                                                                      Lau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                   Human
                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                 Created)
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Pred.
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                                                                                      D.H.P.,
                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                   Two
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No. 2.1e-17;
                                                                                                                                                         Preisig-Mueller
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                                                                   Pore
                                                                                      Zhadina
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                                                                                                                                                                                                                                                                Hominidae;
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DBJ databases.
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Best Local
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                                                                                                                                                                                                                                                    Q9H592 PRELIMINARY;
Q9H592;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TREMBLREL. 1
DJ137F1.1 (NOVEL MEMBER O
Submitted (SEP-2000) to the EMBL; AL136087; CAC07335.1; Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003280; -.
Pfam; PF02034; TWIK_Channel; 1
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
                                                             SEQUENCE FROM N.A. Williams S.;
                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ionic channel SEQUENCE 37
                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                              DJ137F1.1
                                                                                                                                                                                                                                  (FRAGMENT).
                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIEEISPSTLKNSLFPSPISSISPGLHSFTDH
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                                                                                                                                                 Chordata;
Primates;
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16, Last sequence update)
16, Last sequence update)
16, Last annotation update)
0F THE POTASSIUM CHANNEL SUBFAMILY
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                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 342.5; 1911;
Pred. No. 2.7e-7;
B; Mismatches 147;
                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                   Hominidae;
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Job time: 415 sec

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RESULT 15
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                                                                                                                                                                                                                                                       Query Match 16.2%; Score 338; DB 11; Length 313; Best Local Similarity 31.8%; Pred. No. 4.7e-17; Matches 76; Conservative 48; Mismatches 107; Indels
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
2P DOMAIN K+ CHANNEL TWIK-2.
                                                                                                                                                                                                                                                                                                                                                     "TWIK-2, an inactivating 2P domain K+ channel.";
J. Biol. Chem. 275:28722-28730(2000).
EMBL; AF281304; AAG10508.1; -.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20435832; PubMed=10887187;
Patela A.J., Maingret F., Magnone V., Fosset M., Lazdunski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9ERU5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ERU5
                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     Honore E.;
                                                                                                                          192 FLLLPPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 FVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GIPLNLVVL----NRLGHLMQQGVNHWASRLGGT---WQ-DPDKARWLAGSGALLSGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 GIPLEGELLAGVGDQLGTIEGKGI----AKVEDTEIKWNVSQTKIRIISTIIEILEGCVL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 I-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAVL 289
                                                                 137
195 LEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRSLYKVLVTAYLFLGLVAMVLVL 253
                                                                                   173 LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKH 232
                                                                                                                                                                                                          57 YLIIGAAVFKALEQPQEISQRTTIVIOKQTFIAQHACVNSTELDELIQQIVAAINAGIIP 116 | | : | | : | | :::::| | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 STIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQ 105
                                                                                                                                                                                         17 YLALGALLVARLERPHEARLRAELGTLREQLLRHSPCVAAHALDAFVERVLAAGRLGRAV 76
                                                               LLTASAQRLSLLLTH--APLSWLSLRWGWHPQRAARWHLVALLMVIVAIFFLIPAAVFAY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 AA;
                                                                                                                                                                                                                                                                                                                                        313 AA; 34214 MW; A93629568785CD8F CRC64;
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25344 MW; 7AB9FB847F242ECE CRC64;
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Search completed: August 28, 2001, 17:12:46

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Match
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1: /SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSB/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSB/gcgdata/geneseq/geneseqp/AA1983.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1985.DAT:*
6: /SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDSB/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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Gapop 10.0 , Gapext 0.5
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2042
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muscle TASK1; TWIK-related acid-sensitive K+ channopotassium channel; drug screening; hypertens hypotensive; epilepsy; arrhythmia; vascular neurodegenerative disease; ischaemia; anoxia; 29-AUG-2000 (first entry) Modified-site Modified-site Modified-site Modified-site Homo Human potassium channel TASK1 WO200027871-A2 Modified-site sapiens. disease; therapy. Location/Qualifiers 53 /note= 392 /note= 393 383 /note= /note= 'note= "O-phosphorylated" "O-phosphorylated" "N-glycosylated" · "O-phosphorylated" "O-phosphorylated" . human; indocrine disease;

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1998;
08-NOV-1999;
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                                                 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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01-OCT-1998;
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                                                                                                  reproductive or developmental disorders, (e.g. arteriosclerosis, clirhosis, psoriasis, acquired immune deficit, y syndrome, anaemia, asthma, Crohn's disease, microbial or other y cytions, congestive or ischaemic heart disease, Alzheimer's, Parking S or Huntington's diseases, schizophrenia, ovulatory defects, scalar dystrophy). HSPP nucleic acids can be used for the recombinant graduction of HSPP, for detecting HSPP in standard hybridisation and scaplification assays (for diagnosis and monitoring), in gene therapy, us antisense, triplex-forming or ribozyme therapeutics, for detecting related sequence or genetic variations, and for chromosomal mapping. HSPP are also used raise specific antibodies (Ab) and to screen ior agonists and
                                                                                                                                                                                                                                                                                                  HSPP are used to treat or prevent disorders :-sociated with increased activity or function of HSPP. Such diseases : clude cell proliferation (including cancer), inflammation, cardiovascular, neurological,
                                                                                                                                                                                                                                                                                                                                                    human signal peptide-containing proteins HSPI to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial outropic, hepatotropic, neuroprotective, cardiovascular and antiast) to activities, and can be used in gene therapy. HSPPs can be used to revent disorders associated with decreased activity or functive of HSPP. Antagonists of associated with decreased activity or functive of HSPP. Antagonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflemmation and cardiovascular disease -
                                                                      monitor, HSPP-related
                                                                                      antagonists (potential therapeutic agents). 🕮 are used to diagnose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 207-208;
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                                                 and for purification of HSPP
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on C, Reddy
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RESULT AAY87291

AAY87291

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hypotensive; epilepsy; arrhythmia; vascular diseases;
neurodegenerative disease; ischaemia; anoxia; endocrine
muscle disease; therapy.
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RESULT
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KW psyc
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Best Local Similarity
Matches 357; Conserv
AAB18807 standard; Protein; 374 AA.

AAB18807:

22-JAN-2001 (first entry)

Amino acid sequence of a human DKCN1 polype;

Human; DKCN1; potassium channel; cancer; potential disease; depression; cardiovascular disease; inflammatory disease; pain; psychiatric disorder; schizophrenia; neurod. Frative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding a non-inactivating potassium transport channel, designated TASS. of hypertension or dysfunctions of the transport of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSIDSGKVFCMFYALLGIPLTLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rvvlrlkphkagvqwrfagsfyfaitvittigyghaaps
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88.1%;
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Pred. No. 9.3e-
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                                                                                                                                                                                                                                                                                                                                                                                          ASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              'SSV 394
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a member of the potassium channel family. The DKCNI polypeptides and polynucleotides are useful for treating diseases including cancer, pulmonary, cardiovascular, inflammatory or renal diseases, pain, psychiatric disorders including depression and schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis and treatment of cancer, inflammatory and renal disease
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10-FEB-2000; 2000GB-0003112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disease including Alzheimer's, neurological disorders, migraine, epilepsy, sleep-related disorders, erectile dysfunction and alopecia. DKCNI polynucleotides are useful as diagnostic reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human DKCN1 polypeptide. The polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 25; 36pp; English.
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                                                                                                                                                                                                                                                     TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                   kadvpdlqsvcsctcyrsqd--
                                                                                                                           -AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                                                                                                                                                               LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGSAHTTDTASSTAAAGGGGFRNVY
                                                                                                                                                                                                                                                                                                 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
                                                                                                                                                                                                                                                                                                                                         \verb|tlvmfqslgermntfvry|| lkrikkccgmrntdvsmenmvtvgffscmgtlcigaaafsq|
                                                                                                                                                                                                                                                                                                                                                                                                                             qlelvilqsephragvqwkfagsfyfaitvittigyghaapgtdagkafcmfyavlgipl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
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59.0%;
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                                                                                 yggrsvapqnsfsaklaphyfhsisykieeispstlk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1116; DB 21;
Pred. No. 4.2e-113;
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Matches
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Best Local
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                                                                                                                                                                                                                                                                  neurodegenerative disease including Alzheimen's, neurological disomigraine, epilepsy, sleep-related disorders, ectile dysfunction alopecia. DKCNI polynucleotides are useful a vilagnostic reagents detecting mutations in the associated gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides and polynucleotides of the potassium channel family, useful for identifying agonists/antagonists of herapeutic use an diagnosis and treatment of cancer, pulmonary, ordiovascular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; DKCNI; potassium channel; cancer; pult, ary disease; dep cardiovascular disease; inflammatory disease: enal disease; pa psychiatric disorder; schizophrenia; neuroded merative disease; Alzheimer's disease; neurological disorder; ridraine; epilepsy;
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                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory and renal disease -
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                                                                                                                                                                                      Local Similarity
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             TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVL; FFSCISTLCIGAAAFSH 180
                                                       MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELROQELRARYNLSQGGYE
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DB; AAA75887.
tlvmfqslgermntfvryllkrikkccgmrntdvsmenmvtv4ffscmgtlcigaaafsq
                                                                                                              ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DM,
                                                                                                                                                                                                                                               374 AA;
                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                    54.7%; Score 1116; DF 1; 59.0%; Pred. No. 4.2e-1; 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374
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                                                                                                                                                                                                                                                                                                           Alzheimen's, neurological disorders, isorders, is ectile dysfunction and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .ary disease; depression;
                                                                                                                                                                                                  Length 374;
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RESULT
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The present sequence represents tandem pore domain weak inward potassium (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4, TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and proteins are used in screening assays to identify candidate compounds which are potential pesticides or therapeutics. The TWIK channel nucleic
                                                                          New tandem pore domain weak inward rectifying potassium.ion (TWIK) channel nucleic acids and proteins, useful in assays for identifying candidate compounds which are potential pesticides or therapeutics -
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                                                           Claim
                                                                                                                    N-PSDB;
                                                                                                                                                         Francis-Lang HL,
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                                                          5; Page 83-85; 96pp; English.
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                                                                                                                                               Gendreau SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                domain weak inward potassium protein;
5; TWIK6; TWIK7; TWIK1; pesticide; ion
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Jeschke P;
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                                                                                                                                   domain weak inward potassium pr
5; TWIK6; TWIK7; TWIK1; pesticie
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in living cells that can be sticide or the standard primers. TWIK regulation, and their use as pesticide or the standard primers. TWIK hybridisation probes and replication/ampli: The strate monoclonal or primers are useful as immunogens that would specifically and in assays to identically enginetrate animals may be used in studying TWIK channels. They, and for screening animals may be used in studying TWIK channels.
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Pred. No. 1.3( ).
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Luo Y, Gendreau SB,
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glqygagfsphned-
                                                          G---GGGGSAHTTDTASSTAAAGGGGFRNVYAEVLHFQS 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eel--iveivrannrgvsaienatsepnwsfgqsfffastvittigyghvtplsrngklf 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mektsfrfslylfayfmflcsgaavfsyfeapeeralrvklgtavqkflvsnpnvtdadl 98
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SB, Jacobus DA, Tietjen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 379; DB 2
Pred. No. 1e-32;
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   -nihrqvvrvrs 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
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Nauen R,
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Jeschke
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е Р;
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Best Local :
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                  The present sequence represents a mechanical contains a protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly an individual and by riluzole. The protein is used to screen for softic modulators which are useful for treating or preventing diseas, of the heart and nervous systems in humans and animals, e.g. epilepsy rediovascular disease (arrhythmia), neurodegeneration (particular disease contains and muscular disease. The protein itself may be used to these diseases. Antibodies specific for the protein are used to these diseases.

Antibodies specific for the protein are used to these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific modulate
system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mechanically sensitive potassium channel protein; TREK-1; polyunsaturated fatty acid; arachidonic acid; 1:luzole; hart disease; nervous system disease; epileps; cardiovascular disease; arrhythmia; neurodegeneration; ischemia; anoxia; hormone sometion abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A mechanically sensitive potassium channel pro win TREK-1
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                              also as therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mechanically sensitive potassium channe. . ec
specific modulators, potential therapeutic .qen.cs
system disorders
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istifilfgcvlfvalpavifkhiegwsaldalyfvv(')trigfgdyvaggsd--iey
                                                                      FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG
                                                                                                ELERVVLRL-KPHKAGV------QWRFAGSFYFA
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                          ANMVLIGEFSCISTLCIGAAAFSHYEHWTFFQAYYYCFI". TTIGFGDYVALQKDQALQT 216
                                                                                                                                                             mkwktvstiflvv--vlyliigaavfkaleqpqeisqr
                                                    fcilyallgiplfgfllagvgdqlgtif---
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                                                                                                                                                                                                                                                                                                                inhibitors or activator-
                                                                                                                                                                                                       Score 369; Db ...
Pred. No. 1.3e ...
Mismatches
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                                                     akvedtfikwnvsqtkiri
                                                                                                                                    TITTIGYGHAAPSTDGGKV 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eed to screen for ts for heart and nervous
                                                                                                                                                                                                                                            Length 370;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                    42;
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QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTRN

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RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1 polynucleotide AAZ00040. h-TREK1 is a two pore potassium channel. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New two pore potassium channel used for, e.g. treapulmonary, cardiovascular and inflammatory diseases {\sf pulmonary}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-1998;
27-JAN-1998;
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                          ANMYLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
                                                                                                                                                                                         ELERVVLRL-KPHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV 108
                                                                                                                                        FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD------VSM 156
                                                                                                                                                                                                                                                                                                       mkwktvstiflvv--vlyliigaavfkaleqpqeisqrttiviqkqtfiaqhacvns--t
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98EP-0300570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 369; DB 20;
Pred. No. 1.5e-31;
7; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
<del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                         102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      42;
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AAY34133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JAN-1999;
25-FEB-1998;
07-AUG-1998;
                                                      disorders. Nucleotides encoding K+Hnov proteins may be used for identifying homologous or related proteins at the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnov protein and in studying the biochemical pathways associated with it. They may also be used for the recombinant production of K+Hnov protein in the protein cultures.
                                                                                                                                             polymorphisms detected as sequence variants by ween multiple independent clones. Potassium channels have controlled in various cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic a axia with myokymia; cardiac arrhythmia (long OT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical componer. If virtually all cells, it is likely that abnormal potassium channers are also implicated in certain renal, cardiovascular and central nervous system (CNS)
                                                                                                                                                                                                                                                                      K+Hnov proteins have a high degree of homolary channels and may be alpha subunits, which for or accessory subunits that act to modulate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding mammalian K+Hnov (...ussium channel proteins, useful for the diagnosis and tree; (...t of episodic with myokymia, cardiac arrhythmia, epilepsy (...) Bartter's syn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potassium channel; ataxia; arrhythmia; epi cardiovascular disorder; CNS disorder; renulomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 104-105; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-527591/44.
N-PSDB; AAZ11915.
                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human K+Hnov5'7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Curran ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY34133 standard; Protein;
                            Additionally, such nucleotides may be used the treatment of diseases associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            istiifilfgcvlfvalpavifkhiegwsaldaiyfv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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98US-0076687.
98US-0095836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rutter M,
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                           hene therapy protocols for all potassium channels.
                                                                                                                                                                                                                                                                                                                                                                                  'o known potassium
                                                                                                                                                                                                                                                                                                                                    channel activity. K+Hnov59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                  the functional channel,
                                                                                                                                                                                                                                                                                                                                                                                                assium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .order.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .-AEHRALLTRN 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartter's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             syndrome
                                                                                                                                                                                                                                                                           Potential
                                                                                                                                                                                                                                                                                         which were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                    polynucleotide AAZ00039. h-TREK1 is a two pore potassium channel, and the gene maps to human chromosome 1932, between the markers D1S237 and WI5105. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's,
            SCIOKE,
                                                                                                                                                          Claim
                                                                                                                             This sequence is the h-TREK1 polypeptide, encoded by the
                                                                                                                                                                                                                                                                Chapman CG,
                                                                                                                                                                                                                                                                                                                 09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                       02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           WO9937762-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           n-TREK1; two pore potassium channel;
chromosome 1q32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h-TREK1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY28496 standard;
                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                       1999-469126/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ldfykpvvwfwilvglayfaavlsmigdwlrviskktkeevgefrahaaewtan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 istiifilfgcvlfvalpaiifkhiegwsaldaiyfvvitlttigfgdyvaggsd--iey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD------VSM 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eldeliqqivaainagiiplgntsnqishwdlgssfffagtvittigfgnisprteggki 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELERVVLRL-KPHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
            and
                                                                                                                                                                                  pore potassium channel used ry, cardiovascular and inflam
                                                                                                                                                                                                                           AAZ00039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                        Page 24; 44pp; English.
            head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                Meadows
                                                                                                                                                                                                                                                                                                                 98GB-0022135.
98EP-0300570.
                                                                                                                                                                                                                                                                                                                                                       98WO-EP07805
          trauma and neurological disorders including migraine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%;
31.0%;
                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                  and inflammatory diseases
                                                                                                                                                                                                                                                                                        PLC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 363; DB 2
Pred. No. 7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102;
                                                                                                                                                                                              treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                             h-TREK1
                                                                                                                                                                                              of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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Claim 7;

Page

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35pp;

English.

The present sequence is human TREKI (h-TREK) the large a member of the 2P domain potassium channel family of prote. which play a part in the control of resting membrane potential. Moduly on of these channels will therefore affect neuronal excitability, the leading to a modulation

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AAB50044
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      Use of human TREK1 polypeptide, polynucleoties encoding them and modulators of h-TREK1 polypeptides for treated polypepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorder; sleep-related attention deficit disorder; addiction
Huntington's chorea
                                                                                                                                               WPI; 2001-080422/09.
N-PSDB; AAC90412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                     Hervieu GJ,
                                                                                                                                                                                                                                                                                                                                                         01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erectile dystunction; alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's chorea; Huntington's chorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuronal excitability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TREK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB50044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; TREK;
                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIER
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31.0%;
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                                                                                                                                                                                                                                     Randall AD;
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Best Local S
Matches 91
           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy, incontinence, erectile dysfunction or alopecia.
                                  Novel isolated h-TRAAK polypeptides belonging to the potassium channel family of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders,e.g. depression and schizophrenia -
                                                                                                                                                                                                                                                                                                                                        2P domain potassium channel; neurodegenerative disease; st psychiatric disorder; neurological disorder; Gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain
                                                                                                                                    Chapman CG,
                                                                                                                                                                                          03-NOV-1998;
07-OCT-1999;
                                                                                                                                                                                                                                03-NOV-1999;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     Human; h-TRAAK; potassium channel polypeptide;
                                                                                                                                                                                                                                                                                                                                                                                                 Human h-TRAAK polypeptide #1
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                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM PLC
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                                                                                            2000-365583/31.
)B; AAA27105.
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         3; Page 21; 35pp; English
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31.0%;
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Pred. No. 7e-31;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                        neurodegenerative disease; stroke;
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                                                                                                                                                                                                                                                                                                                                                                                           Human; h-TRAAK; potassium channel polypeptid
2P domain potassium channel; neurodegenerat
psychiatric disorder; neurological disorder in neurological disorder
Chapman CG,
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                                                                                                                                                                                                                                            11-MAY-2000
                                                                                                                                                                                                                                                                                                 WO200026253-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human h-TRAAK polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY94426 standard; Protein; 393 AA.
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                                                  (SMIK ) SMITHKLINE BEECHAM
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                                                                                                       98GB-0024048.
99GB-0023668.
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31.0%;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  disease; stroke;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                  Mechanically sensitive potassium channel protein; TRAAK; polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease; nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     schizophrenia, neurodegenerative disease including Alzheimer's, s and head trauma and neurological disorders including migraine and epilepsy. The present sequence is human h-TRAAK protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and chiscabers, such as pain, psychiatric disorders including depression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Pages 21 and 22; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated h-TRAAK polypeptides belonging to the potassium chamily of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders, e.g. depression and schizophrenia -
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N-PSDB; AAA27106.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AA;
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                                                                                                                                                                                              (first entry)
                                                                         ischemia;
                                                                                                                                                                                                                                                                     Protein;
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31.0%; Pred. No. 2.9e-27;
tive 43; Mismatches 112
                                                                                                                                                                                                                                                                                                                                                         291
                                                                       anoxia; hormone secretion abnormality;
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Matches 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1; 40pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mechanically sensitive potassium channel of the specific modulators, potential therapeutic descriptions system disorders
                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                             ----VAFSFVYILTGLTVIGAFLNLVVLR 245
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                                                                                                                                                                                                                               LALIVCTFTYLLVGAAVFDALESEPELIBRORLEL-RG: TATALENGGYEELERVVL 67
                                                                                                                                                                                                                                                                                                                                                                                                       as therapeutic inhibitors or activator.
lvwfwilfglayfasvlttignwlravsrr
                                                         g---cllfvltptfvfsymeswskleaiyfvivtlttv4
                                                                                       GFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGIC: \\VALQKDQALQTQPQY--
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US-08-256-242-4
US-09-351-215-2
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US-09-351-215-4
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US-09-352-084-12
US-09-353-125-2
US-09-351-215-13
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US-09-351-392-6
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  RESULT 2
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
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; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2
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Best Local Similarity
Matches 91; Conser
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CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street,
ATTORNEY/AGENT INFORMATION:
                                                                     CURRENT APPLICATION DATA:
                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                 CLASSIFICATION:
                                    APPLICATION NUMBER: FILING DATE: 15-NO
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Lazdunki, Michel
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                                  15-NOV-1996
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Best Local Similarity 32.4
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5559026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08332312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Versior
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3246
                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                REFERENCE/DOCKET NUMBER:
                                              REGISTRATION NUMBER: P-38,711
                                                                                                               FILING DATE:
                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: American Cyanamid Company
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVII
                                                             Harrington, James
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Pausch, Mark H.
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INFORMATION FOR SEQ ID NO:

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SEQUENCE CHARACTERISTICS:

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; MOLECULE TYPE: protein US-08-332-312-2
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                     TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James,
REGISTRATION NUMBER: p-38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Price, Laura A. APPLICANT: Pausch, Mark H. TITLE OF INVENTION: Melanag
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 -----GYMYIILLYIILGKF 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 LAILIVY-----TAFGGVLMSKLEPWSFFTSFYWSFITMTTVGFGDLMP-RRD------ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 NMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 GERI-----NTL-VRYLL---HRAKK-----GLG-----MRRADVSMA 157
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                                 TOPOLOGY:
                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Wayne
                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                LENGTH:
                                                                                                                                        TELEPHONE:
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                                               : 618 amino acids amino acid
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Pred. No. 9.1e-20;
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Score 231.5;

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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383
                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 SMANMYLIGEFSCISTL-CIGAAAFSHYEHWTFFQAYYYYFTFUTTIGFGDYV-ALQKDQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 KVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKK--
                                                                                                                                                                                                                                                                                                                                     STREET: Zov C. CITY: Philadelphia
                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                  TELEFAX:
                                                                     REFERENCE/DOCKET NUMBER:
                                                                                    NAME: Weiser, Gerard REGISTRATION NUMBER:
                                                                                                                                           CLASSIFICATION:
                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 15-NOV
                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGSAHTTDTASSTAAAGGGGFRNVYAEVLHFQSMCSC:\\TKSREKLQYS---IPMII 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKEFGGWFVVYQIFVIVWFIFSLGYL--VMIMTFITRGL:
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230 South Fifteenth Street, Suite 5:0
                                                                                                                                                                                                                                                                                                                      USA
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Barhanin, Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                    215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duprat, Fabrice
Lazdunki, Michel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fink, Michel
                                                                                                                                                                                                             PatentIn Release #1.0, Version !1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lesage, Florian
                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                            15-NOV-1996
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                                                                                                   Gerard J
ID NO:
                                                                                                                                           536
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                                                                                    19,763
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                                                                       989.6351P
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-749-816-4
                                                                                                     US-08-749-816-3
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US-09-236-080-4
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Sequence 3, Application US/08749816
Patent NO. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEO ID NOS: 6
SOFTWARE: FASTSEO for Windows Version 3.0
SEO ID NO 4
LENGTH: 107
TYPE: PRT
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APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
                                                                                                                                                                                                                                                                                                                                              Query Match 8.6%; Score 176.5; DB Best Local Similarity 33.0%; Pred. No. 5e-12; Matches 34; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09236080 Patent No. 6242217
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Best Local Similarity 24.0
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6242217el Compounds FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164
                                                                                                                                                                                                                          138 YLLHRAKKGLGMRRAD-------VSMANMVLIGFFSCI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 TKKLILMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVIPVGYGYIFPVSAYGR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                                                                                                                                                                                                                WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIF- 67
                                                                                                                                                                                                                                                                                                        WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCLIAYALLGIPLTLVTMADTGKFAAQLV-----TRWFGDNNMAIPAAIFVCLLFAYP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --RVVLRLK-PHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l: 383 amino
amino acid
                                                                                                                                                                                    -GKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCV 102
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-749-816-3
                                                                                                                                                           US-08-288-405A-10
                                                                                                Sequence 10, Application US/08288405A Patent No. 5559009
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
                                           APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                APPLICANT:
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ADDRESSEE: WEISER &
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                           APPLICANT:
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                                                                                                                                                                                                                                      201 YLIFLSSLLLCSISLLSSSALFSSIENISYLSSVYFGIITMFLIGIGDIV
                                                                                                                                                                                                                                                                                                                                                  114 ALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADV ;MAN--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk.

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version.
                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31
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ZIP: 19102
                                                                                                                                                                                                                                                                                                                                                                                                                       60 EELERVYLRLKPH------KAGVQWRFAGSFYFAITVITT1;YGHAAPSTDGGKVFCMFY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RONVRTLALIVCTFTYL---LVGAAVFDALESEPELIERO. ELROQELRARYNLSQGGY 59
                                                                                                                                                                                                                                                                       --MVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCF11LTTIGFGDYV
                                                                                                                                                                                                                                                                                                            SLLMIPVFIAFKFEFGTFLAHFLVVVSNRTR--LAVKKAYYKLSQNPENAETPSNSLQHD
                                                                                                                                                                                                                                                                                                                                                                                       ----KITAEMKSKLGKCLTKSSRIDGFGKAIFFSWTLYSTVGYGSLYPHSTLGRYLTIFY 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RQNVNVVVCLSAAITLLVFNLIGAGIFYLAETQN---SSES; NENSEVSKCLHNLPIGG- 86
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230 South Fifteenth Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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VENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
VENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE
VENTION: OF DRUGS
                                           Chandy,
                                                           Kalman,
                                                                              Chandy,
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, Kanianthara G.
, Katalin
, Grischa
, George A.
, A No. 5559009el Voltaço
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TITLE OF INVENTION:

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.Potassium Channel

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TITLE OF INVENTION: GOURNESS OF SEQUENCES: CORRESPONDENCE ADDRESS

ADDRESSEE:

Embarcadero Center, Suite 3400

Flehr, Hohbach, Test, Albritton & Herbert, Attn: Walter H. Dreger

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                   SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 2, Applic Patent No. 5986081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                     CURRENT APPLICATION NUMBER: US/08/956,242C CURRENT FILING DATE: 1997-10-22 NUMBER OF SEQ ID NOS: 13
                                                                                                                                      TITLE OF INVENTION: Polynucleotides Encoding Herg-3 FILE REFERENCE: 960296.94550
                                                                                                                                                                      APPLICANT: Ganetzky, Barry S. APPLICANT: Titus, Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: '10: SEQUENCE CHARACTERISTICS:
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                     412 DRV----DTHFTSI----PESFWWAVVTWTTVGYGDMAPVTVGGKIVGSLCAIAGVLTIS 463
                                                                                                                                                                                                                                                                                                                                    464 LPVPVIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 RASMRELGLLI---SFLFIGVVLFSS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGI---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 5.0%;
Local Similarity 22.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/207,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RONVRTLALIVCTFTYLLYGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEEL 62
                                                                                                                                                                                                                                                                                                                                                                    -PLTLVMFQSLGERINTLVRYLLHRAKKG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
                                                                                                                                                                                                                                               Application US/08956242C
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Pred. No. 0.0085;
7; Mismatches 3
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US-08-464-340A-4

Sequence 4, Application US/08464340A Patent No. 5710019

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, NAME/KEY: unsure
; LOCATION: (441)..(542)
; OTHER INFORMATION: Uni
US-08-956-242-2
                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: unsure
; LOCATION: (441)..(542)
; OTHER INFORMATION: Uni
US-09-351-215-2
RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ganetzky, Barry S.
APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding
FILE REFERENCE: 960296.94550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1997-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/956,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                     121 TLVMFQSLGERINTLVRYL 139
                                                     374 -SLMYASIFGNVSAIIQRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 LELLMCTFALIAHWLACIWYAIGN----VERPYLEHKIGKI SLAVQLGKRYNGSD---- 325
                                                                                                                                                             61 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAFSfDGGKVFCMFYALLGIPL 120
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                                                                                                                                                                                                                     9 LALIVCTFTYLLVG-AAVFDALESEPELIERQRLELR----
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                                                                                                                         -PASGPSVQDKYVTALYFTFSSLTSVGFGNV: UNTNSEKVFSICVMLIG---
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23.7%;
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23.7%; Pred. No. 0.0
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                                                                           RESULT
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                 Sequence 4, Application PC/TUS9408449A GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US94/08449
FILING DATE: 28 JUL 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
 APPLICANT:
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                447
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CITY: R
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REFERENCE/DOCKET NUMBER: 325800-415
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                                                                                                                                                                                                                                                                                                                                                                                  TLVMFQSLGERINTLVR-YLLHRAKKGL-----GMRRADVSMANMVLIGFFSCISTLCIG 174
                                                                                                                                                                HTTDTASSTAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYS---IPMI 328
                                                                                                                                                                                                                                    SFVYILTGLTVIGAFLNLVVLRFMTMNAEDE -- KRDAEHR-ALLTRNGQAGG-GGGGGSA 279
                                                                                                                                                                                                                                                                          ALGYTMEQSHPE--TLFKNIPQSFWWAIITMTTVGYGDIYPKTTLSKLNA-----AI 389
                                                                                                                                                                                                                                                                                                              AAAF----SHYEHWTFF----QAYYYCFITLTTIGFGDY---VALQKDQALQTQPQYVAF 223
                                                                                                                                                                                                                                                                                                                                                TNVQQAVQALRIMRIARIFKLARHSSGLQTLTYALKR---SFKELGLLLMYLAVGIFVFS 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERVVLRL--KPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                SDLDNLPPEPAG - -
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US-08-956-242-4
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GENERAL INFORMATION:
                 Sequence 4, Application US/08956242C Patent No. 5986081
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PCT-US94-08449A-4
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Best Local :
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NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,
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INFORMATION FOR SEQ ID NO: 4:
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FILING DATE: SUBMITT
CLASSIFICATION:
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                           283 TNVQQAVQALRIMRIARIFKLARHSSGLQTLTYALKR---SFKELGLLLMYLAVGIFVFS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ARVVAELSFLLILVSSVVMCMDTIPELQVLDAEGNRVEH: . . .----NVETACIGWFTL 235
                                        280 HTTDTASSTAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYS---IPMI 328
                                                                                                                                                                                                                                                                                                                                               236 E-YLLRLFSSPNKL----HFALSFMNIVDVLAILPFYVSN:...THLGARM------MEL 282
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                                                                                                                                                                                                                                                                                                                                                                                      63 ERVVLRL--KPHKAGVQWRFAGSFYFAITVITTIGYGHA TO TDGGKVFCMFYALLGIPL 120
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TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
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                                                                                                                                                                                              AAAF----SHYEHWTFF----QAYYYCFITLTTIGFGDYX<sup>II</sup> VALQKDQALQTQPQYVAF 223
                                                                                                                                                                                                                                                                                       TLVMFQSLGERINTLVR-YLLHRAKKGL-----GMRRADV: MANMVLIGFFSCISTLCIG
                                                                                                                            SFVYILTGLTVIGAFLNLVVLRFMTMNAEDE--KRDAEH, ALLTRNGQAGG-GGGGGSA 279
                                                                                                                                                                       ALGYTMEQSHPE--TLFKNIPQSFWWAIITMTTVGYGUL KTTLSKLNA-----AI
SDLDNLPPEPAG-
                                                                                 SF----LCGVIAIALPIHPIINNFVRYYNKQRVLETAAKHELELMELNSSSGGEGKTGGSR
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CURRENT APPLICATION NUMBER: US/08/956,242C
CURRENT FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 888
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APPLICANT: Titus, Steven A.
ITTLE OF INVENTION: Polynucleotides Encoding
FILE REFERENCE: 960296-94550
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LOCATION: (133)
OTHER INFORMATION: Unidentified at time
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ORGANISM: Homo sapien
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OTHER INFORMATION:
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OTHER INFORMATION: Unidentified
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Sequence 4, Application US/09351215 Patent No. 6087488 GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956,242
EARLIER FILING DATE: 1997-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ganetzky, Barry S.
APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding Herg-3
FILE REFERENCE: 960296.94550
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SOFTWARE: PatentIn Ver.
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TYPE: PRT
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OTHER INFORMATION: Unidentified at time of filing
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OTHER INFORMATION: Unidentified at time of filing
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Sear	Db	Qy	Db	Qy	Db
Search completed: August 28, 2001, 17:06:23 Job time: 527 sec	339 LRORLEEYFOHAWTYINGIDM-NNVLKGFPECLQADICL 376	147 LGMRRADVSMANMYLIGFFSCI-STLCI 173	283 EKIFSICVMLIGSLMYASIFGNVSAIIQRLYSGTARYHMQMLRVKEFIRFHQIPNP 338	106 GKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG 146	236 QQIGKRYNDSDSSSGPSIKDKYVTALYFTFSSLTSVGFGNVSPNTNS 282

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Title:
Perfect score:
Sequence: OM protein - protein search, using sw model Scoring table: Run on: US-09-503-089A-5
2042
1 MKRQNVRTLALIVCTFTYLL....STGLHSLSTFRGLMKRRSSV 394 August 28, 2001, 17:07:05 ; Search time 36.66 Seconds (without alignments) 818.679 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	1	No.	Result	
	229	231.5	231.5	234.5	235.5	239.5	243	244	245	247.5	248	250	251	251	256.5	258	258.5	259.5	261.5	262	268	275	293	307.5	320.5	599	599	806.5	820	Score		
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	325	519	484	485	475	522	528	381	769	392	444	569	576	544	452	383	427	335	1001	443	1539	524	393	513	336	364	334	336	329	Length		
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	T15584	T16629	T43529	T24201	T27725	T24265	T21834	T43393	T27550	T45032	T26229	T43531	T43363	T43364	T21118	T23182	T27681	S44635	T13807	T21598	T30037	T23907	T25392	T28933	S65566	T43361	T19860	T32347	T43509	IB		
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185	189.5	190.5	193.5	199.5	200.5	201.5	201.5	205.5	210	210.5	211	215.5	216	222.5	229
9.1	9.3	9.3	9.5	9.8	9.8	9.9	9.9	10.1	10.3	10.3	10.3	10.6	10.6	10.9	11.2
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ALIGNMENTS

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Oy 295 of Db 293 RESULT 2 T32347 Outward res C; Species: C; Date: 29, C; Accessio	Qy 1 Db 1 Qy 2 Db 2	0y Db Db 1	probable po C;Species: C;Date: 21 C;Accession R;Wang, Z.I submitted: A;Referenco A;Accession A;Status: 1 A;Molecule A;Residues A;Cross-re A;Cross-re	RESULT T43509
Oy 295 GFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLETSNTCVEQSHSSPGGG 350 : :	179 SHYEHWTEFQAYYYCFITLTTIGFGDYVALQKDQALQTU ZYYAFSFVVILTGLTVIGAF 238	1 MKRONVRTLALIVCTETYLLVGAAVFDALESBPELIEF. FIROGELRARYNLSOGGYE 60	probable potassium channel chain n2938 - Caenorit. 1.1s elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-202	

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R;Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F34D6.
A;Reference number: Z21153
A;Accession: T32347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-336 <*MUR>
A;Residues: 1-336 <*MUR>
A;Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
A;Gene: twk-23; CESP:F34D6.3
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                        RESULT
T19860
                                                                                                                                                                                                                                                                                      hypothetical protein C40C9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T19860
                                                                             A; Gene: CESP:C40C9.1
A; Map position: X
A; Introns: 34/1; 60/2;
                                                                                                                              A; Experimental source: C; Genetics:
                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-334 <WIL>
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                                                                                                                                           Cross-references: EMBL:Z70266; PIDN:CAA94204.1; Experimental source: clone C40C9
                                                                                                                                                                                                         Status: preliminary; translated
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Best Local :
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Best Local Similarity
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Local Similarity
nes 119; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 MSNADYEILEATIVKSVPHKAGYQWKFSGAFYFATTVITTIGYGHSTPMTDAGKVFCMLY 120
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 Conservative
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                                                                             98/1; 145/3; 160/3; 181/1;
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               29.3%;
                                                                                                                                                                                                                                                          Library,
46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 806.5;
Pred. No. 5.5e
54; Mismatches
               Score 599; DB 2; Pred. No. 5.1e-47;
                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                          March
Mismatches
                                                                                                                                                                                                           GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                       15-Oct-1999 #text_change
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                                                                              204/1;
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81;
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                          Length 334;
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Indels
                                                                             252/2;
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12;
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Gaps
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R:Wang, Z.W.; Salkoff, L. submitted to the EMBL Data Library, I A;Description: Potassium channels in A;Reference number: 222450
A;Accession: T43361
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C;Date: 11-Jan-2000
C;Accession: T43361
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A; Residues: 1-364 <WAN>
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243 SACVNLLVLGFMASNADE 260
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29.3%; Score 599; DB
Local Similarity 46.1%; Pred. No. 5.7e-
es 119; Conservative 46; Mismatches
4 QNVRTLALIVCTETYLLVGAAVFDALESEPELIERQRLL
2014
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                                                                                                                                                                                                                                              YMEHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIMFILIGLAVF
                                                                                                                                                                                                                                                                                                                     AAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALOK&QYVAFSFVYILTGLTVI
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inward rectifier potassium channel TWIK-1 - human C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997
C;Accession: \$65566
R;Lesage, F; Guillemare, E; Fink, M; Duprat, F;
EMBO J. 15, 1004-1011, 1996
A;Title: TWIK-1, a ubiquitous human weakly inward x

human weakly inward rectifying K(+)

channel with a

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Barhani nove

M.; Duprat, F.; Gazdunski, M.; Romey,

#text_change 05-Nov-1999

RESULT S65566

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C; Accessic
R; Nelson,
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T28933
hypothetical protein C52B9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t.
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A;Accession: S65566
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-336 <LES>
A;Cross-references: EMBL:U33632; NID:g1086490;
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                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9 A;Experimental source: strain Bristol N2; clone C52B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: T28933
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Best Local Similarity
Matches 105; Conserv
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                                                                                           VKNMFQAYRNQFITAKHLLNKTREDEVLWTFPNSMFFAATVITTIVQVKNRSGNRVVFSR 172
                                                                                                                                                                                      LALIVCTFTYLLVGAAVFDALESEPEL-----IERQRLELRQQELRARYNLSQGGYEEL 62
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                                                                                                               ERVVLRL------KPHKAGVQWRFAGSFYFAITVITTI------
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                             GYGNLVPITVTGRVACIIFALLGIPLLLVTIADIGKFLSEFLSY-LYRSYRGFKRKLRRQ
                                                           GYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMR----
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                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                      Score 307.5; DB:
Pred. No. 3.9e-20
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hypothetical protein R04F11.4 - Caenorhabditis C; Species: Caenorhabditis elegans C; pate: 15-Oct-1999 *sequence_revision 15-Oct-1 C; Accession: T23907 R; Harris, B.
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A; Residues: 1-393 <WIL>
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 submitted to the EMBL Data Library, June 1996
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                                                                                                                                                                                ITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVI. AFLNLVVLRFM 247
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                                                                                                                                                    ITMTTVGFGDIVPLKR----
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                                                                                                                                                                                                                                            -AKKGLGMRRADVS---MANMYLIGFFSCI----STLCIG, \ \FSHYEHWTFFQAYYYCF 194
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78; Conserv
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ilarity 26.6%;
Conservative 5
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%; Pred. No. 6e-1
57; Mismatches
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A;Reference number: Z19816
A;Accession: T23907
A;Status: preliminary; translat
A;Molecule type: DNA
A;Cross-references: EMBL:Z74475
A;Cross-references: EMBL:Z74475
A;Experimental source: clone R(C;Genetics:
A;Gene: CESP:R04F11.4
A;Map position: 5
A;Introns: 35/3; 83/2; 131/1; 1
                                                                                                                                                                                                                                                                                                    hypothetical protein F20A1.7 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30037
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                                                                                                                                                       A;Cross-references: EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN00023; A;Experimental source: strain Bristol N2; clone F20A1
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                                                                                                                                                                                                                                 A; Reference number: A; Accession: T30037
                                                                                                                                                                                                                                           submitted to the EMBL Data Library, March A;Description: The sequence of C. elegans A;Reference number: Z20726
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                            Local Similarity 24.0 Local Similarity 24.0
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8 TLALIVCTFTYLLVGAAVFDALESEPELIERQ------RLELRQQELRA-RYNLSQGG
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                                                                                                 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3;
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                         Score 268; DB 2
Pred. No. 6.2e-1
60; Mismatches 1
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Pred. No. 3.8e-17;
8; Mismatches 92
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126;
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R; Mortimore, B. submitted to the EMBL Data Library, *.pafarance number: Z19447.
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A; Map position: 5
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A; Residues: 1-443 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 13/3; 90/2; 149/1; 222/3; 290/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSAAVFCLFEDWTFFTSFYFCFISLTTIGLGD-----VTPANPEYMIATFGVVIVG
                                    IGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGA: _NI VVLRFMT----MNAEDEKR
                                                                             EMKEIERQERHDLDIFDLPLPVGIALIVTWIFICSFVLSVWDHNWTLLESFYFFFTSLST
                                                                                                                                                                PMTDAGRMLTMIFALFGIPLMLLVLQDFGKLLTITMKFFWFOIKRLMRRIMRCCTKQPIE 192
                                                                                                                                                                                                         PSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHFAKKGL-----
                                                                                                                                                                                                                                                    KGNTSQRLTTFFIEELGSYEN----QLGVKWSQQKMDWDFWNAVLFAGTICTTIGYGHIY 132
                                                                                                                                                                                                                                                                                                                                  LIIVFLIYCISGGLVFWLIEEPYQSELRDAWQHKIENNEFARVDAMMKKIFNNSDYLIYI 76
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                                                                                                                                                                                                                                                                                                                                                                                                                      78;
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                                                                                                                       -GMRRADVSMANMVL-IGEFSCISTLCIGAAAFSHYEH-WTFFQAYYYCFITLTT 199
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-PSSPRLLITMFGFILVGLSLVSN: !NL!OAKMKSTYEAGRNDEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%;
25.0%;
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No. 4.7e-i5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 443;
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C; Genetics: A; Introns:
                                                                                                                                                                                    submitted to the EMBL Data A; Description: Sequence of A; Reference number: $44628
                                                                                                                                                                                                                                                 f22b7.7 protein - Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Date: 20-reb-1995 #sequence_revision 20 C;Accession: S44635
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A;Status: preliminary; translated
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A;Title: ORK1, a potassium-selective leak channel with two po A;Reference number: 217770; MUID:97075152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
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A; Residues: 1-335 <AND>
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                                                                                                          A;Cross-references: EMBL:L12018; NID:g156298;
                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                       A; Accession: S44635
                                                                                                                                                                                                                                       R; Anderson, K.
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Query Match
Best Local S
Matches 60
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IALIPGIALFLLLPSWVFTYFENWPYSISLYYSYVTTTTIGFGDYVPTFGANQPKEFGGW
                                                                             18/3;
60; Conserv
                                                                             79/1; 131/2;
   Conservative
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              12.7%;
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the C. elegans
                                                                             173/3;
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Pred. No. 1.4e-15;
5; Mismatches 107;
Score 259.5; DB 2
Pred. No. 5.7e-16;
1; Mismatches 50
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                                                                             251/3
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                             DB 2;
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Indels
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49;
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hypothetical protein K01D12.4 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1 C;Accession: T23182
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Gene: CESP: ZK1067.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross·references: EMBL:Z70038; PIDN:CAA93881.1; A;Experimental source: clone ZK1067
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A; Residues: 1-427 <WIL>
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A; Reference number:
                submitted to the EMBL
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                                                                                                                                                                                                                                                                                                                                                                                             195 TFTSINFRAFKEGLKPTDFLVPQETSRWSMISAIFFTTTVLTSIGYGNLIPISTGGKIFC
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                                                                                                                                                                                                                                                        -MTISACVYTILEPMWSFLDSFYFCLVSLLTVGFGD
                                                                                                                                                                                                                                                                                       TLCIGAAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQP----QYVAFS
                                                                                                                                                                                                                                                                                                                            VGYALFGIPLTLVTIADLAKFVADMLIMDPTEDPKTGRCL---
                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LRLKPHKAGV-----
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Pred. No. 9.4
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                                                                    15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T23182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-383 <WIL>
A;Cross-references: EMBL:275543; PIDN:CAA99871.1; G:
A;Experimental source: clone K01D12
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A;Map position: X
A;Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3
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A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2
                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:278541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:F19D8 A;Experimental source: clone F19D8
                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-452 <WIL>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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93 IAKLATTENVAE--INEHLRMFLRNISNLHISLDNYLIFNEPTQIVPKR----WTFPSSV 146
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                                                                                                         MKRQNVRTLAL-----IVCTFTYLLVGAAVFDAL--ESEPELIERQR---LELRQQ- 46
                                      MKFRNVLRIALGHLALYCFVVC---YVFAGAWVFHQLEGENETELHDKQREYAMNLKKDV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYVSNQQDVTRMSPDLYRFVNFCLLTLGACFFYCLSNVSSIVVRQLLNWMIKK-MDVKVE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYVALQKDQALQTQPQY------VAFSFVYILTGLT--VIGAFLNLVVLRFMTMNAE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCGGHMDNWRPSVYKVFFILFSMCLVLITASAGIYSVVENWNYIDSLYFCFISFATIGFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEMVRFI--SDGATSGLLNSRSRFDHLGSLFFSATVISTIGFGTSTPRTHLGRFITIVYG 157
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                                                                                                                                                                                    12.6%; Score 256.5; DB 2 28.6%; Pred. No. 1.5e-15;
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                                                                              CFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTC , VIGAEL 239
                                                                                                                KGLGMRRADVSMAN-------MVLIGFFSCISTLC AAFSHYEH-WTFFQAYYY 192
                                                                                                                                                              LFSFTILTTIGYGNVTPHTQQCKVFLMIYGAFGIPLFL1: ADLGRESKTAIMALVQKVS
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Search completed: August 28, Job time: 475 sec 2001, 17:07:06

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Result
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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CIW1_MOUSE
CIW6_HUMAN
ORK1_DROME
TWK8_CAEEL
CIW7_HUMAN
CIW8_MOUSE
                                                                                                                                                                                                                                                                                                                                                                        CIW2_HUMAN
CIW4_HUMAN
CIW4_MOUSE
CIW1_HUMAN
HERG_HUMAN
WC2C_ARATH
CIK6_HUMAN
CIK5_RAT
CIK4_HUMAN
                                                                                                                                                TAGC_DICDI
YWS1_CAEEL
A2AR_LABOS
IFR1_MOUSE
Y139_METJA
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WC2A_ARATH
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IFR1_RAT
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CIW3_MOUSE
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054912 rattus norv
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NAT. Neurosci. 2:422-426(1999).

-I. FUNCTION: PH-DEPENDENT, VOLTAGE-INSENS. V. BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTI.: PASULIS FROM POTASSIUM CONCENTRATION ON EITHER SIDE OF THE CHANREL ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIVE OF NCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION: V. THE CUBRENT IS INWARD.

-I. SUBCELLULAR LOCATION: INTEGRAL MEMBRAN. V. THE (POTENTIAL).

-I. TISSUE SPECIFICITY: WIDESPREAD EXPRESS V. AULIT. STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. L. V. XINFESSION IN BRAIN, LUNG, PROSTATE, HEART, KINNEY, UTERUS, J. L. INTESTINE AND COLON.

-I. MISCELLANEOUS: INHIBITED BY EXTERNAL AV. V. ATTION. ACTIVATED BY HALOTHANE AND ISOFLURANE.

-I. SIMILARITY: BELONGS TO THE TWO PORE DO. AMILY OF POTASSIUM CHANNELS.
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                InterPro;
InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99254548; PubMed-10321245;
Patel A.J., Honore E., Lesage F., Fink M., G., Lazdunski
"Inhalational anesthetics activate two-porchain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBO J. 16:5464-5471(1997).
[2]
                                             MIM; 603220;
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               IPR000099;
IPR001622;
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Lazdunski M.; eckground K+

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and the EMBL outstation -

in no way

HUMAN FINDARD; PRT; 394 AA. CIW3_HUMAN STANDARD; PRT; 394 AA. O14649; O1-OCT-2000 (Rel. 40, Created) O1-OCT-2000 (Rel. 40, Last sequence update: O1-OCT-2000 (Rel. 40, Last sequence update: POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (AC - C - C - C - C - C - C - C - C - C -

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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
KONK3 OR TASK.
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TISSUB-Cerebellum;
MEDLINE-98099797; PubMed-9437008;
Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H.,
Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
"An open rectifier potassium channel with two pore doms
                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
MCBI_TaxID=10116;
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PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01333; 2POREKCHANEL.
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InterPro; IPR003092; ...
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InterPro; IPR003280; ...
InterPro; IPR003280; ...
IPfam; PF02034; TWIK, Channel; 1.
PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01333; ZPOREKCHANEL.
Ionic Channel; Transmembrane; Ic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cloned from rat cerebellum.";
J. Neurosci. 18:868-877(1998)
-:- FUNCTION: PH-DEPENDENT, V
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                                          YEHWIFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQ 📚 ESFVYILTGLTVIGAFLN
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE F CONTINET)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rroton block and voltage gating are cardiac leak channel kcnk3.";
J. Biol. Chem. 275.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim D., Fujita A., Horio Y., Kurachi Y "Cloning and functional expression of background K+ channel (cTBAK-1)."; Circ. Res. 82:513-518(1998).
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                                                                                                                                                                                                    modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duprat F., Lesage F., Fink M., Reyes "TASK, a human background K+ channel near physiological pH.";
EMBO J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4-409 FROM N.A. MEDLINE-97459932; Pubmed-93
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                                                                                                                                                                              entities
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Kim D., Fujita A.,
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Mammalia; Eutheria; Rodentia;
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- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIT CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE, ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARN
                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRALN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.

MISCELLANBOUS: INACTIVATED BY BARIUM.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
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                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY
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.M., Gallagher P.G., Buck M
                                                                                                                                                 requires a license agreement (S
an email to license@isb-sib.ch).
; BAA25436.1;
; AAC53367.1;
; BAA28349.1;
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re potassium-dependent
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DT 01-CCT-2000 (Rel. 40, Created)

DT 01-CCT-2000 (Rel. 40, Last sequence update) i

DT 01-CCT-2000 (Rel. 40, Last annotation update i

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SEQUENCE FROM N.A., F
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                                                                                                                                                                                                                                                                                                                                           Ionic channel; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fink M., Duprat
Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, functional expression and unconventional outward rectifier K+
                                                                                      SEQUENCE
                                                                                                                                       DOMAIN
                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02034; TWIK_channel; 1. PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channels."
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"Inhalational anesthetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99254548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 15:6854-6862(1996).
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"Cloning, functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fink M., Duprat
                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRED LEMBRANE PROTEIN (POTENTISUE SEPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG.

DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: INHIBITED BY BARIUM.
ANAESTHETICS SUCH AS CHLOROFORM, DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
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e E., Lesage F., Fink M.,
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                   Score 370; DB 1;
Pred. No. 2.1e-22;
                                                                                                                                                     SENSITIVITY
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PORE-FORMING
                                                                                                                                      REQUIRED FOR BASAL CHANNEL ACTIVITY
                                                                                                                                                                         ESSENTIAL FOR
                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                           PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                             Ion transport;
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-LINKED (GLCNAC. . .)
8F976DDD103EFA05 CRC6
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTASSIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fink M., Romey G., Lazdunsk.
two-pore-domain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          brain localization
channel.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                       CHLOROFORM AND HALOTHANE
   126;
                                                                                                                                                                                                                                                                                                                                                             Potassium transport;
                               Length 411
                                                                                      CRC64;
   Indels
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ID LUNG. ALSO
NOT DETECTED
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                                                                                                    (POTENTIAL)
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                                                              use by non-profit institutions as long a
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entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                     Price L.A. Hellings S.E., Hayashi J.H., Pa::ch M.H.:
Submitted (MAY-1997) to the EMBL/GenBank/DD: darabases.
-!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
-!- SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                      This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=99254548; PubMed=10321245;
Patel A.J., Honore E., Lesage F., Fink M.,
"Inhalational anesthetics activate two-por
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANNEL SUBUNIT).
                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channels."
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                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Neurosci.
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                                                                                                                     s SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics European Bioinformatics Institute. There are the swiss and the swiss institute.
                                                                                                                                                                                                                         SUBCELLULAR LOCATION: INTEGRAL MEMBRANE FROTEIN (POTENTIAL) MISCELLANBOUS: ACTIVATED BY VOLATILE GEREAL ANAESTHETICS SUCHLOROFORM, HALOTHANE AND ISOFLURANE.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN! AMILY OF POTASSICIANMETS.
                                                                                                                                                                                                                CHANNELS
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                                        email to license@isb-sib.ch).
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two-pore * main background
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ackground K+
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Best Local
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CONFLICT
SEQUENCE
                                                                          01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                           Homo sapiens (Human).

--- Metazoa; Chordata;
        SEQUENCE FROM
                         NCBI_TaxID=9606;
                                                                   KCNK4 OR TRAAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                        282 LDFYKPVVWFWILVGLAYFAAVLSMIGRLVRVISKKTKEEVGEFRAHAAEWTAN
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                                                                                                                                                                                                            QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTRN
                                                                                                                                                                                                                                                  ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
                                                                                                                                                                                                                                                                                                                                   ELERVVLRL-KPHKAGV------OWRFAGSFYFAITVITTIGYGHAAPSTDGGKV 108
                                                                                                                                                                                                                                                                                                                                                       MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T
                                                                                                                                                                                                                                                                                                                                                                          MKRONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                            FCIIYALLGIPLFGFLLAGVGDQLGTIF----
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                                                                                                                                                                                                                                                                                                                ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 172
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003280;
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         N.A.
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                                                                                                                                        STANDARD;
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                                      Primates;
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30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                             61;
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N-LINKED (GLCNAC...) (PO)
MISSING (IN REF. 2).
RLV -> DWL (IN REF. 2).
S -> N (IN REF. 2).
A -> T (IN REF. 2).
W; 2ABA2336D4009F4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 6.7e-22;
l; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 364; DB 1; Pred. No. 6.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REQUIRED FOR BASAL CHANNEL ACTIVITY
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                                      Catarrhini;
                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ion transport;
                                                                                                                                        PRT;
                                                                                                                                       393
                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                      Hominidae;
                                                                                                                                                                                                                                                                       -GKGIAKVEDTFIKWNVSQTKIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 426;
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                                      Homo
                                                                                      ARACHIDONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport;
                                                                                                                                                                                                                                                                                                                                                                                              42;
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Best Local
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Chapman C.G., Meadows H.J., Godden R.J., Carribell D.A., Duckworth M. Kelsell R.E., Murdock P.R., Randall A.D., P. un e.G.L., Gloger I.S., "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassis hannel.";
Brain Res. Mol. Brain Res. 82:74-83(2000). [7]
[2]
SPOITENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is proved through a collable between the Swiss Institute of Bioinformation, and the EMBL outst the European Bioinformatics Institute. The the no restrictions use by non-profit institutions as long and scenarios in modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF248242; AAG31731.1; EMBL; AF247042; AAF64062.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See htra://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Assignment of KCNK4 encoding the human potase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gray A.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Frontal
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                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: VOLTAGE INSENSITIVE,
                   224
                                          177
                                                                                           124
                                                                  164
                                                                                                                   114
                                                                                                                                           67
                                                                                                                                                                    57
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                                                                                                                                                                                                                9 LALIVCTFTYLLVGAAVFDALESEPE-LIERQRLELRQQE| KARYNLSQ-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTERNAL K+ CONCENTRATIONS (BY SIMILARIT SUBURIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE 'SIMILARITY: BELONGS TO THE TWO PORE DOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTASSIUM CHANNEL, OUTWARD RECTIFICATION OF REXTERNAL K+ CONCENTRATIONS
                                                                                                           ALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRKA
                                                                                                                                                                                         LALLALVLLYLVSGALVFRALEQPHEQQAQRELGEVREKE, AHPCVSDQELGLLIKEVA
                   SFVYILTG----
                                                                                                                                         DALGGGADPETNSTSNSSHSA---WDLGSAFFFSGTII: YGNVALRTDAGRLFCIFY
                                         LIGCLLEVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGFGBYVAGADPR--QDSPAYQPL
                                                                FFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGF; BYVALQKDQALQTQPQYVAF
                                                                                        ALVGIPLFGILLAGVGDRLGSSLRH-----GIGHIEA : KWHVPPELVRVLSAMLFL
                                                                                                                                                                 ---GGYEELERVVLRLKPHKAGVQWRFAGSFYFAITVITI . YGHAAPSTDGGKVFCMFY
                                                                                                                                                                                                                                           98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR01333;
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001622;
                                                                                                                                                                                                                                          Conservative
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118
140
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171
192
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LTVIGAPLNLVVLRPMTMNAEDDES JABEHRALLTRNGQAGGGGGG
                                                                                                                                                                                                                                                     16.1%;
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                                                                                                                                                                                                                                                       Score 329.5;
Pred. No. 3.4
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N-LINKED (GLCNAC. .) (
N-LINKED (GLCNAC. .) (
P -> L (IN REF. 2).
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PORE-FORMING
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PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
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                                                                                                                                                                                                                                           Mismatches
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PORE DOMA 9 "AMILY OF POTASSIUM
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hes 112;
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                                 Glycoprotein;
DOMAIN
                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-F STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIW4_MOUSE O88454;
                  TRANSMEM
                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A neuronal two P domain K+ channel polyunsaturated fatty acids."; EMBO J. 17:3297-3308(1998).
                                                                                                                                                               EMBL; AF056492; AAC40181.1;
                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCNK4 OR TRAAK
                                                           Ionic
                                                                        PRINTS;
                                                                                      Pfam; PF02034; TWIK_channel; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                        [nterPro;
                                                                                                                    [nterPro;
                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fink M., Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98292450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inhalational anesthetics activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276
                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPELICING.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE.
DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS CHLOROFORM, DIETHLE ETHER, HALOTHANE AND ISOFTURANE.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARD POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTERNAL K+ CONCENTRATIONS
                                                                                                                                                   MGI:1298234;
                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASWTGTVTARVTQRAG
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                                                           S; PR01333; 2POREKCHANEL. channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurosci.
                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
                                                                                                     IPR003280; -
                                                                                                                                  IPR000099;
                                                                                                                      IPR001622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
HANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED
 ; Alternative : 1 3 4 24 89 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2:422-426(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                Kcnk4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=9628867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291
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                                           splicing
POTENTIAL.
PORE-FORMING (POTENTIAL)
                              CYTOPLASMIC (POTENTIAL).
                                                           Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heurteaux C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fink M., Romey G., Lazdunsk
e two-pore-domain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stimulated
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                                                           Potassium
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EVERSED AT HIGH
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                                                                                                                                                                                                                                                                    EMBL outstation
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RESULT 8
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Best Local Similarity
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01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
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CARBOHYD
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DOMAIN
                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hom., NCBI_TaxID=9606;
                                                                                                                                                                                                                                                       01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update
POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWA CHANNEL SUBFAMILY K MEMBER 1 (INWA CHANNEL K $5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC VARSPLIC
   Desir G.V., Orias M., Submitted (APR-1997)
              SEQUENCE FROM Desir G.V., On
                                         J. Mol.
                                                                   MEDLINE=98122696;
Goldstein S.A.N.,
                                                                                        TISSUE=Brain;
                                                                                                SEQUENCE FROM
                                                                                                                     EMBO
                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                 KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
                                                                                                                                                                                                                                                                                                                  CIW1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                              novel structure
                                                                                                                                                          Lesage F.,
                                                                                                                                                                   MEDLINE=96183184;
                                                  implications
                                                                                                                                      "TWIK-1, a ubiquitous human
                                                          Soldstein S.A.N., Wang K.-W., Ilan Northern Sequence and function of the two P
                                                                                                                                                                                                                                                                                                                                                                  235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVWFWILFGLAYFASVLTTIGNWLRAVSRR
                                                                                                                                                                                                                                                                                                                                                                                    ----VAFSFVYILTGLTVIGAFLNLVVLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRA--
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                                                                                                                                                                                                                                                                                                                                                                                                        ·CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGF 7624--PGDGTGQNSPAYQP
                                                                                                                                                          Guillemare
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140
172
198
235
256
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84
63
                                   of an emerging superfamily."; 76:13-20(1998).
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                      N . A .
                                                                                                N.A.,
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                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                    PubMed=8605869;
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                                                                                                 AND
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31.5%;
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Freeman T.;
to the EMBL/GenBank/DDBJ databases.
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H
                                                                                                 REVIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                       weakly inward restricting
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Pred. No. 6.1e-1
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                                                                                                                                                          Duprat F
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                                                                                                                                                                                                                   Hom .uidae;
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                                                          potassium
                                                                                    M. C. C.
                                                                                                                                                                                                                                                                                          KARYNLSQGGYEELERVVL
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د.
                                                                     M.H.;
                                                                                                                                                          Lazdunski M.,
                                                                                                                                                                                        OF THR-161
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                                                                                                                                                                                                                              Euteleostomi;
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                                                            channels:
                                                                                                                                        K+ channel with
                                                                                                                                                                                                                                                                    POTASSIUM
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                                                                                                                                                          Romey G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 9
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Best Local
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MUTAGEN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U33632; AAB01688.1; -. EMBL; U76996; AAB97878.1; -. EMBL; U90065; AAB51147.1; -. MIM; 601745; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001622;
InterPro; IPR001779;
InterPro; IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                          230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HE
BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
SINILLARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHANNELS
                                                                              TG----LTVIGAFLNLVVL---RFMTMNAEDEKRDAEH
                                                                                                                                  AAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVA----LQKDQALQTQPQYVAFSFVYIL
                                                                 LGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVH
                                                                                                                                                                  LLFLTAVVQRIT-----VHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIP
                                                                                                                                                                                          LVMFQSLGERINTLVRYLLHRAKKGL------GMRRADVSMANMYLIGFFSCISTLCIG
                                                                                                                                                                                                                      SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT
                                                                                                                                                                                                                                                                      LVLGYLLYLVEGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA
                                                                                                                 AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR01096; TWIK1CHANNEL. PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                       104
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  20
41
130
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177
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267
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38143
                                                                                                                                                                                                                                             -QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLT
                                                                                                                                                                                                                                                                                                                                     15.7%;
                                                                                                                                                                                                                                                                                                                                                                                         W.
                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                     Score 320.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTT->A: NO EFFECT ON CHANNEL; 2A41D9501323215D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      PORE-FORMING (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PORE-FORMING POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ion transport; Potassium
   PRT;
                                                                                                                                                                                                                                                                                                                         Mismatches
   499
                                                                                                                                                                                                                                                                                                                                     .5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
   ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                         102;
                                                                 292
                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transport;
                                                                                                                  YKIGITCYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN HEART
                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in no way
                                                                                                                                                                                             174
                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                         85
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                                                                                                                                                                   199
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Best Local S
Matches 84
                                                                                                                                 TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACI. 51.5
CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID-CENS.)
                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is probetween the Swiss Institute of Bioinformatic the European Bioinformatics Institute. Then
                                                                                                                                                                                                                                                                  Pfam; PF02034; TWIK_channel; 1 PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                       SEQUENCE
                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                              Glycoprotein.
                                                                                                                                                                                                                                                                                                  InterPro; IPR001622;
                                                                                                                                                                                                                                                                                                                         MIM; 603493;
                                                                                                                                                                                                                                                                                                                                    EMBL; AF084830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and expression of a novel pH-sensi: channel from human kidney.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reyes R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99030343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                              InterPro; IPR000099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        [onic channel;
                                                                                                                                                                                                                                                                                         [nterPro;
                        15
   67
                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANF PERFEIN (POTENTIAL).

TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                               CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACIDIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K+ CONCENTRATIONS.
--LRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAP: (*** KVFCMFYALLGIPLTLVM
              YLAIGAAIFEVLE-EPHWKEAKKNYYTQKLHL----LK'
                                           YLLVGAAVFDALESEPELTE ---- RQRLELRQQELRA . . .
                                                                          Similarity
                                                                                                                                                                                                                                                                                        IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duprat F.,
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                                                                  Conservative
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                                                                                                                       8
                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                    AAC79458.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=9812978;
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Primates;
                                                                                                                       55130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lesage F., Fink M.,
                                                                 15.6%; Score 319; Did 32.8%; Pred. No. 3.1: ...
Live 47; Mismatches
                                                                                                                        MW.
                                                                                                                                                            PORE-FORMING (1 TTIAL).
POTENTIAL.
CYTOPLASMIC (P. IAL).
POTENTIAL.
PORE-FORMING (+, MFIAL).
                                                                                                                                POTENTIAL.
CYTOPLASMIC (PCTTVIAL).
N-LINKED (GLCNT).
                                                                                                                                                                                                                        CYTOPLASMIC (PC')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertor ta; i
Catarrhini; Home idae;
                                                                                                                                                                                                                                                        Ion transport; Lotassium transport;
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                                                                                 Length 499;
                                                                 ...
                        .:LGQEGLDKILEVVSDAAG
                                                                                                                                                                                                                                                                                                                                                                                                            and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                    ://www.isb-sib.ch/announce/
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                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTERNAL
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                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O08581;
O08581;
O1-OCT-2000 (Rel. 40, Createu,
O1-OCT-2000 (Rel. 40, Last sequence upon correction)
O1-OCT-2000 (Rel. 40, Last annotation)
OTASSIUM CHANNEL SUBFAMILY K MEMBER J
between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.ish-cib.ch.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KCNKI.

Mus musculus (Mouse).

Mus musculus (Mouse).

""karyota; Metazoa; Chordata;
""karyota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure, chromosome localization, mouse twik K+ channel gene.";
FEBS Lett. 425:310-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=129/SVJ; TISSUE=Liver; MEDLINE=98218573; PubMed=9559671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIW1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The structure, function and distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lesage F., La
Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97165959; PubMed=9013852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION IN
KIDNEY. THYROLD, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
EXPRESSION IN EYES, PITUTTARY, PANCREAS, SMOOTH NUSCLE, TES
                                                                                                                                                                                                           MISCELLANEOUS: INHIBITED BY QUI
ACIDIFICATION. ACTIVATED BY PRO
SIMILARITY: BELONGS TO THE TWO
                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE:
CONCEPTION. EXPRESSION STABILIZES AFTER DAY
                                                                                                                                                                                                                                                                                                                                                           OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL MUSCLE, TEXTI.

CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPIG AND SPICEN.

CORTEX.
                                                                                                                                                                                          CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WKVSMFVEVHKAIKKR
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                                                                                                                                                                                                                                                                                                             EXPRESSION
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                                                                                                                                                                                                                                                                                                                                EXPRESSION
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                                                                                                                                                                                                                                                                                                        INCREASES
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                                                                                                                                                                                                           Y QUININE,
Y PROTEIN I
                                                                                                                                                                                                                                                                                                        S FROM 2-8
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R 1 (INWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Carle G.F., and tissue d
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WINASE C.
DOMAIN FI
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                                                                                                                                                                                                           C.
FAMILY
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; Murinae; Mus
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                                                                                                                                                                                                             OF POTASSIUM
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                                                                       no
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RESULT 11
CIW6_HMMAN STANDARD; PRT; 313 AA.
ID CIW6_HMMAN STANDARD; PRT; 313 AA.

Q9Y257;
AC Q9Y257;
DT 01-CCT-2000 (Rel. 40, Created)
DT 01-CCT-2000 (Rel. 40, Last sequence update)
DT 01-CCT-2000 (Rel. 40, Last annotation update)
DT 01-CCT-2000 (Rel. 40, Last annotation update)
DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 6 (INWARD RECTIFYING DE CHANNEL PROTEIN TWIK-2) (TWIK-ORIGINATED SIMILARITY SEQUEN KCNK6 OR TWIK2 OR TOSS.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
          Pountney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes D., Saganich M., Rudy B., Artman M., Coetzee W.A.:
"Identification and cloning of TWIK-originated similarity sequence (TOSS): a novel human 2-pore K+ channel principal subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01096; TWIK1CHANNEL. PRINTS; PR01333; 2POREKCHANEL.
                                         MEDLINE=99285568; PubMed=10359073;
Pountney D.J., Gulkarov I., Vega-Saenz de Mieta E.,
                                                                             SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=9606;
[1]
                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02034; TWIK_channel;
                                                                   TISSUE=Testis;
                                                                                                                  Mammalia;
                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                    146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LIVCTFTYLLVGAAVFDALESEPELIERQRL-ELRQQELRARWNLSQGGYEELERVVLRL 69
                                                                                                                                                                                                                                                                                          LGLITMLVVLETFCELHELKKFRKMFYVKKDKDEDLVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:109322; Kcnkl.
Lett.
                                                                                                                                                                                                                                                                                                                TG-
                                                                                                                                                                                                                                                                                                                                       AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYN
                                                                                                                                                                                                                                                                                                                                                            AAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVA----LCI AALQTQPQYVAFSFVYIL
                                                                                                                                                                                                                                                                                                                                                                                    LLFLTALVQRVT-----VHVTRRPVLYFHIRWGFSKQVV8.VHAVLLGFVTVSCFFFIP
                                                                                                                                                                                                                                                                                                                                                                                                           LVMFQSLGERINTLVRYLLHRAKKGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPHKAGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEPHECLSEPQLEQFLGRVLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF033017; AAC16973.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003280; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001622; -. IPR001779; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000099;
novel human 2-pore K+ channel 450:191-196(1999).
                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                LTVIGAFLNLVVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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104
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268
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41
130
153
177
198
238
267
336
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                                                                                                                  Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                REMIMNAEDEKRDAE
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PORE-FORMING (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 318.
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (P.
                                                                                                                  Catarrhini;
                                                                                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A996060A18266FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318.5;
No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                           -GMRRADV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2e-18;
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                                                                                                                  Hom
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                                                                              idae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             otassium transport;
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                                                                                                                                                                SEQUENCE)
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                                                                                                                                                                                                                                                                                                                                       YKIGITCYLL
                                                                                                                                                                         POTASSIUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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Mehta Y., Forsayeth J.R., Yost C.S.;
J. Biol. Chem. 274:24440-24440(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mehta Y., Forsayeth J.R., Yost C.S.;
"TWIK-2, a new weak inward rectifying
potassium channel family.";
                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF1177
MIM; 603939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -I- SUBCHLULAR HOMODIMER (POTENTIAL).
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
-I- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETEC
TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chavez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99175162; PubMed-10075682;
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SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001622;
InterPro; IPR001779;
                                                                                                                                                                                                                                                 MUTAGEN
                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ionic channel; Transmembrane;
                              121
                                                                                                                                                                            Local
                                                         74
                                                                                 64
                                                                                                            17
                                                                                                                                       18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS. LOWEST EXPRESSION DETECTED IN BRAIN.
MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                      YLLVGAAVFDALESEPELIERQRLELRQQELRARYN----
TMLLLTASAQRLSLL---LTHVPLSWLSMRWGWDPRRA----ACWHLVALLGVVVTVCFL
                           TLVMFQSLGERINTLVRYLLHRAKKGLGM-----RRADVSMANMVLIGFFSCISTLC--
                                                       RVVLANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPT
                                                                                                            YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAG----RLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF134149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF117708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.A., Gray A.T.,
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           PR01096; TWIK1CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chem. 274:7887-7892(1999)
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121
142
173
199
236
257
79
85
85
313
                                                                                                                                                                  Conservative
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AAD24000.1;
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25
115
114
172
193
223
223
223
256
313
79
85
85
33747
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                                                                                                                                                                               14.5%;
31.7%;
                                                                                 WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao B.B.,
, Yost C.S.
                                                                                                                                                                                                                                      ₹.
                                                                                                                                                                  40;
                                                                                                                                                                              Score 295.5;
Pred. No. 1.
                                                                                                                                                                                                                                   N-LINKED (GLCNAC...) (PO
N-LINKED (GLCNAC...) (PO
C->A: NO CHANNEL ACTIVITY.;
1379382DFB0575DE CRC64;
                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kindler C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kindler C.H., Mazurek M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   member of the tandem pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRONGEST EXPRESSION IN
                                                                                                                                                                1.4e-16;
hes 95;
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                               Potassium
                                                                                                                                    ------LSQGGYEELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DETECTED IN ALL
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                                                                                                                                                                  Indels
                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                 (POTENTIAL)
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                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                               transport;
                                                                                                                                                                                            313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                  59;
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                                                                                                                                                                Gaps
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commercial
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 186
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RESULT 12
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            RA Ballew R.M., Basu A., Baxendale J., Bayrakt, Julu L., Beasley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhanchald D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu J., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu J., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J., Detz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J., Detz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J., Detz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J., Detz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor J.,
RA Cherry J.M., Cawley S., Dahlke C., Ferraz C., F., Lang W., Houck J.,
RA Harris M.L., Harvey D., Heiman T.J., Hernanc J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernanc J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernanc J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernanc J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernanc J.R., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori S.J., MoShrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori S.J., MoShrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori S.J., MoShrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.K., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.K., Pacleb J.M.,
RA Nelson D.R., Siden K., Saunders R.D.C., Schen B.C., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Skiir A., M.P., Smith T.,
RA Shier E., Spradling A.C., Stapleton M., Kollysenbach J.,
RA Williams S.M., Woodsey T., Moriey R., Shen H., Wools Senbach J.
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Ye J., Yeh ĸ. ..,
Zheng X.H., Zhong F.N.,
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01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
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Eukaryota; Metazoa; Arthropoda; Tracheata; ': ::oda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nidchycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Amanatides P.G., Scherer S.E., Li P.W.,
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                        Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGE
EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW
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SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF
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genome sequence of Drosophila melanogaster.";
nce 287:2185-2195(2000).
                                                                                          FVVYQIFVIVWFIFSLGYL--VMIMTFITRGLQSKK
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RESULT 14

CIN7_HUMAN STANDARD; PRT; 3

ID CTW7_HUMAN STANDARD; PRT; 3

AC Q9Y2U2; Q9Y2U4; Q9Y2U3;

DT 01-0CT-2000 (Rel. 40, Created)

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DT 01-0CT-2000 (Rel. 40, Last annotation

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is provided through a collable between the Swiss Institute of Bioinformatics There is the European Bioinformatics Institute. There is the European Bioinformatics Institute. There is the European Bioinformatics Institute is as long as the content is in modified and this statement is not removed. The content is in entities requires a license agreement.
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MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae;
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TWK-8 OR F22B7.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                WormPep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L12018; AAA65460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                     185
                                                                                                                                                             219
                                                                                                                                                                                                                                                                      129
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                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                               MVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFIT! : 3FGDYVALQKDQALQTQP
                                                                                                                                                                                                                                                                                            VKKNAATETWTFSSSIEFAVTVVTTIGYGNPVPVTNIGH
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                                                                                                                                                                                                                                            GKFLSEHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHS/ NIGHDMNIEEKRIPAFLVL
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335 AA; 38472
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(Rel.
(Rel.
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28, Last sequence update)
36, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                               12.7%;
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                                                                                                                                                                                                                                                                                                                                                               Score 259.5;
Pred. No. 1.1(
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                             update)
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               update
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                                                                                                                                                                                                                                                          G-----MRRADVSMAN 158
                                                                                                                                                                                                                                                                                    LESLIGIPLTLVTIADL
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                                                                                                                                                                                                                                                                                                                                                    ; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                     CRC 64;
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בינבי, Staden
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                                                                                                                                                                                                                                                                                                                                                     49;
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Best Local
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                                                                                                                                                                                          VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of a new mouse two-P domain channel subunit and a human homologue with a unique pore structure.";
J. Biol. Chem. 274:11751-11760(1999).

-i- FUNCTION: PROBABLE POTASSIUM CHANNEL SUBUNIT. NO CHANNEL ACTIVITY OBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICULUM.
MAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER TO
                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99223496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001622;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                              VARSPLIC
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             121
                                    73
                                                         69
                                                                                 13
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO
ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                       LIVCTFTYLLVGAAVFDALESEP--ELIERQRLELRQQELRARYNLSQGGYEELERVVLR 68
            TLVMFQSLGE---
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                                   TQAHGVSTLGNSSEGRTWDLPSALLFAASILTTTGYGHMAPLSPGGKAFCMVYAALGLPA 132
                                                                                LVVAHLLALGLGAVVFQALEGPPACRLQAELRAELAAFQAEHRACLPPGALEELLGTALA 72
                                                                                                                               Similarity
77; Conserv
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307
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                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
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R., Lesage F., F
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31946 MW;
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257
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307
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252
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Pred.
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(IN ISOFORM C).
MISSING (IN ISOFORM
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N-LINKED (GLCNAC. . .) (
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                                                                                                                                                                                                                                                                                                                                                                                                              Ion transport; Potassium transport;
..
                                                                                                                                                                                         ISSING (IN ISOFORM C).
BD4A36DD9591ADAC CRC64;
                                                                                                                               Mismatches
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                                                                                                                                          224; DB 1;
No. 6.8e-11
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                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                -> GGTSLQGTAWEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HERE),
                                                                                                                                                     Length 307
                                                                                                                                                                                                                 B).
> KSSHLTACGGRGKRSLD
                                                                                                                               Indels
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C.
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                                                                  TISSUES.";

SUBMITTED

- FUNCTION: PROBABLE POTASSIUM CHANNEL SUJINITY. NO CHANNEL ACTIVITY

- FUNCTION: PROBABLE POTASSIUM CHANNEL SUJINITY. NO CHANNEL ACTIVITY

OBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICULUM.

MAY NEED TO ASSOCIATE WITH AN AS YET UNATAN PARTNER IN ORDER TO

REACH THE PLASMA MEMBRANE.

- SUBUNIT: HOMODIMER (POTENTIAL).

- TISSUE SPECIFICITY: DETECTED IN EMBRYO,

WEAKLY EXPRESSED IN COLON, TESTIS, ATRIA, IDNEY, INTESTINE,

BLADDEE, UTERUS, OVARY, SALIVARY GLAND, MUS AND BRAIN STEM, NO

BLADDEE, OTERUS, OVARY, SPENAL CC. HEART, VENTRICLE,

WEAKLY EXPRESSED IN COLON, SPINAL CC. HEART, VENTRICLE,

BLADDEE, UTERUS, OVARY, SPINAL CC. HEART, VENTRICLE,

BLADDEE, SPINAL CONTROL 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9Z2T1; Q9Z242; Q9RIVI; Q9QYE8; Q9QXYO; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) 01-OCT-2000 (Rel. 40, Last annotation update) POTASSIUM CHANNEL SUBFAMILY K MEMBER 8 (PUTATE IN DP3) (DOUBLE-PORE K+ CHANNEL 3) (NEUROMUSCULAR IN
                                                                                                                                                                                                                                                                                                                                                                                                                 Gan L., Joiner W.J., Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bockenhauer D., Gallagher P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain, and MEDLINE=99223496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIW8_MOUSE
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                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
Lopes C.M.B.,
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 15-307 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tshibashi K.,
"Cloning of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning of a new mouse two-P domain chann-
homologue with a unique pore structure.";
J. Biol. Chem. 274:11751-11760(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salinas M., Reyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                             "A new two P domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
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                               DETECTED IN BRAIN, CEREBELLUM, SPINAL CC. HEART, VENTRICLE, SKELETAL MUSCLE, LIVER, PLACENTA AND PAN "EAS. IN THE EYE, HIG EXPRESSED IN THE RETINAL GANGLION CELL I." R AND INNER NUCLEAR
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLGYLLLGLLAMLLAVETFSELPQVRAMGKFFRPSGPV. AEDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLALVATLRHCLLPVLSRPRAWVAVHWQLSPAR-----
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237 ALLGYLLLGLLAMLLAVETFSELPQVRAMVKFFGPSGSRTDEDQD
                           221 VAFSFVY--ILTGLTVIGAFLNLVVLRFMTM-----NAEDEKRD 257
                                                                                164 FFSCISTICIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQ---KDQALQTQPQY 220
                                                                                                         127 ALGLPASLALVAALRHCLLPVFSRPGDWV--AIRWQLAPAQAAL-----LQAAGLGLL-
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MGS -> TR (IN REF. 4).

GS -> TH (SR REF. 4).

GS -> THSREFGPRGQEFGTR (IN REF. 2).

G -> S (IN REF. 2, 3, 4 AND 5).

YH -> SP (IN REF. 2).

T -> P (IN REF. 2).

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Search completed: August 28, 2001, 17:13:15 Job time: 409 sec

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Best Local Similarity
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InterPro; IPR001622; -.
InterPro; IPR003092; -.
InterPro; IPR003092; -.
InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01395; TASKCHANNEL.
                Q9ESM4
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SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gan L., Joiner W.J., Quinn / Kaczmarek L.K.; Submitted (SEP-1997) to the EMBL; AF022821; AAD09338.1;
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01-MAY-2000
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Pred. No. 7
                PRT;
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Sciurognathi;
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Matches 256;
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01-MAR-2001 (
01-MAR-2001 (
01-MAR-2001 (
TWIK-RELATED
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Girard C., Lesage F.,
"Human Task-3, a novel
Submitted (JUN-2000) t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTASSIUM CHANNEL KCNK9.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                         SEQUENCE FROM N.A
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"TWIK-related acid-sensitive K+
                                                                                                           MEDLINE=20287530;
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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56; Conservative
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
D ACID-SENSITIVE K+ CHANNEL SPRICE VARIA
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the EMBL/GenBank/DDE.
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Pred. No. 8.8e
6; Mismatches
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Catarrhini; Hominidae;
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Best Local Similarity
Matches 233; Conserv
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InterPro; IPR000099; -.
InterPro; IPR001622; -.
InterPro; IPR003092; -.
InterPro; IPR003092; -.
InterPro; IPR003380; -.
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
IONIC Channel
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J. Biol. Chem. 275:16650-16657(2000).
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BMBL; AF2579809; AAF6370801; -.

EMBL; AF257080; AAG33126.1; -.

EMBL; AF248241; AAG31730.1; -.
Q9JL58
Q9JL58;
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Vega-Saenz de Miera E.C.,
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KT3.2 and KT3.3 o
TASK1.";
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          PRELIMINARY;
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Pred. No. 1.5e-90;
4; Mismatches 96;
          PRT;
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Query Match 52.4
Best Local Similarity 57.1
Matches 226; Conservative
                               Q9JLD4; PRELIMINARY; Q9JLD4; 15 01-OCT-2000 (Tremblrel 15 01-OCT-2000 (Tremblrel 15 01-MAR-2001 (Tremblrel 16 POTASSIUM CHANNEL TASK3.
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InterPro; IPR001622; ...
InterPro; IPR003092; ...
InterPro; IPR003280; ...
InterPro; IPR003280; ...
Pfam; PP02034; TWIK, Channel; 1.
PFANTS; PR01333; ZPOREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
SEQUENCE 365 AA; 40769 MW; 2
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01-OCT-2000
01-MAR-2001
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extracellular histidine as pH sensor."
J. Biol. Chem. 275:16650-16657(2000).
EMBL; AF212827; AAF63706.1; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20287530; PubMed=10747866; Rajan S., Wischmeyer E., Liu G.X.,
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Pred. No. 1.9
43; Mismatches
                                            Created)
Last sequence up
Last annotation
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Hystricognat) (idae;
Craniata; Ver
Sciurognathi
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Best Local Sim
Matches 174;
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NON_TER 2:
SEQUENCE 23:
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TWO PORE POTASSIUM CHANNEL KT3.2 (FRAGMENT)
                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY;
Vega-Saenz de Miera E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01333; 2PONEKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
SEQUENCE 395 AA; 44365 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kim Y., Bang H., Kim D.;
"TASK-3, a New Member of the Tandem
J. Biol. Chem. 275:9340-9347(2000).
                                                                                                                                                                Submitted (APR-2000) to the EMBL; AF257082; AAG33128.1;
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                                                                                                                                                                                                                              "KT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9ES08;
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[1]
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                                                                                                                                                                                                                            zee W., Rudy B.;
.2 and KT3.3 Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVLRFMTMNAEDEKRDAEHRALLTRN
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26674 MW;
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73.4%;
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                                                                                                                                                                                     EMBL/GenBank/DDBJ
                     Score 924;
Pred. No. 8
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                                                                                                                                                                                                                                                                      D.H.P.,
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Q9H427;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                           Submitted (APR-2000) to the EMBL; AF257081; AAG33127.1; Ionic channel. SEQUENCE 330 AA; 36130 MW
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
TWO PORE POTASSIUM CHANNEL KT3.3.
                                                                                                                                                                                                                                                                                                                                     Coetzee W., Rudy
"KT3.2 and KT3.3
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Vega-Saenz de Miera E.C.,
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Primates;
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Catarrhini;
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01-MAR-2001
PUTATIVE POT
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EMBL; AL118522; CAC14068.1; -
SEQUENCE 330 AA; 36222 MW; 24F428721A1C779
                                                                                                                                                          Wang Z.-W., Salkoff L.; "Potassium channels in C. el Submitted (AUG-1998) to the EMBL; AF083552; AAC32863.1;
                                                                                                                                                                                                                                Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
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Mammalia; Eutheria;
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                                                                               Ionic channel.
SEQUENCE 329
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DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE
                                                                                                      PRINTS;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                              InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1.
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MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
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                                                                                                    PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                            998 (TrEMBLrel. 08, Created)
998 (TrEMBLrel. 08, Last sequence update)
001 (TrEMBLrel. 16, Last annotation updat
POTASSIUM CHANNEL SUBUNIT N2P38.
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                       Conservative
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                 40.2%;
                                                                              36992 MW; 338A6D9A577464CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                              258
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                                                                                                                                                                                     elegans.";
                                                                                                                                                                                                                                             Caenorhabditis.
                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
                     Score 820; DB
Pred. No. 1.8e
54; Mismatches
                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 838;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24F428721A1C7790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                      329
                      ..8e-64;
les 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
.8e-66;
                                                                                                                                                                                                                                                                                                                                       Ą
                                            BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60;
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                                                                                                                                                                         databases.
                                         Length 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 330
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                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                                      Rhabditoidea;
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                      46;
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017185;
01-JAN-1998
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01-MAR-2001
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Wilson R., Ainscough R., Anderson K., Bayne:
Bonfield J., Burton J., Connell M., Copsey J., Coulson Craxton M., Dear S., Du Z., Durbin R., Favc.
Gardner A., Green P., Hawkins T., Hillier I., Fulton L., Johnston L., Johnston L., Johnston J., Kirsten J., Lister N., Jarreille P., Lightning J., Lloyd C., Mcmurray A., Morting J., O'Callaghan M., Parsons J., Percy C. Rifken I., Popper A., Morting J., Percy C., Rifken I., Popper A., Morting J., Percy C., Rifken I., Popper A., Marting J., Percy C., Rifken I., Percy C., Per
                                                                                                                  Submitted (SEP-1997) to the EMBL; AF025454; AAC71151.1; InterPro; IPR000099; -. InterPro; IPR001622; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Cae
                           InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel;
PRINTS; PR01333; 2POREKCHANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parsons J., Percy C., Rifken L., Roop
Smaldon N., Smith A., Sonnhammer E.,
Thierry-Mieg J., Thomas K., Vaudin M.
Watson A., Weinstock L., Wilkinson-Sp
   SEQUENCE
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegans
                                                                                                                                                                                                                                           Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
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tson A., Weinstock L., Wilkinson-Sproat J.
2 Mb of contiguous nucleotide sequence !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLIMFQSIGERMNTFAAKLLRFIRRAAG-KQPIVTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                           Wohldmann (SEP-1997)
   336
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   AA;
                           2POREKCHANEL.
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37700
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the EMBL/GenBank/DD:
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Last annotation update)
                                                                                                                                                                                                            EMBL/GenBank/DDRJ
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   E0474024F69FC27E
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                                                                                                                                                                                                            Jacabases
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   CRC64;
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                   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorlova M., Bays A.D., Dew I., Dietz S.M.,
RA Dorlova M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Halush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2000
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIE------RQRLELRQQELRARYN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGG
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 14, Last annotation
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RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., "Sissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter F.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter R.,
RT "The genome sequence of Drosophila melanog. S., Zhu X., Smith H.O.,
REILBEG. EBEJ.03760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 166; Conser
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Q9VFS9;
01-MAY-2000 (TrE
01-MAY-2000 (TrE
01-JUN-2000 (TrE
CG9637 PROTEIN.
                                                                                                                          Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexipoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera: Pachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                      CG9637
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Interpro; IPR003092; -.
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01095; TASKCHANNEL.
SECULENCE 340 AA; 37840 MW;
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InterPro; IPR000099; -.
InterPro; IPR001622; -.
STRAIN-BERKELEY;
MEDLINE-20196006;
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291
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                                                                                                                                                                                                                                                                                       ) (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
  PubMed=10731132;
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RA Abrill J.F., Dayayani A. An H.-J. Andrews-Pfannkoch C.K., MISIOS G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Davies P., Davies P
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Best Local Similarity
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InterPro; IPR001022; ...
InterPro; IPR001092; ...
InterPro; IPR001092; ...
PFAm; PF02034; TWIK_channel; 1.
PRINTS; PR01095; TASKCHANNEL.
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                                                                                                                                             -LTRNGQAGGGGGGGSAHTTDTA 285
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OCCOOC OC	JI บรูบ	Db Qy
Olimar-2000 (TIEMBLIE) Olimar-2001 (TIEMBLIE) ENARY-2011 (TIEMBLIE) ENARY-2012 (TIEMBLIE) Cavia porcellus (Guinea pig). Mammalia; Eutheria; Rodentia; Hystricog McBILINE-2028750; Pubmed-10747866; Rajan S., Wischmeyer E., Liu G.X., Prei Rajan S., Marker Prei Rajan S., Wischmeyer E., Liu G.X., Prei Rajan S., Marker Prei Rajan S., Marker Prei Rajan S., Marker Prei Rajan S., Prei Rajan S.	329 HIRHLLPEVVPMODLN 344 LT 14 57 O9JL57 PRELIMINARY: PRT: 270 A O9JL57; PRELIMINARY: PRT: 270 A O1-OCT-2000 (TrEMBLrel 15, Created) O1-OCT-2000 (TrEMBLrel 15, Last sequence	YSIPM

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SEQUENCE
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Science 282:2012-2018(1998).
EMBL; AF083646; AAG32857.1; -.
EMBL; 270266; CAB61045.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLREL SUBUNIT NZP20.
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Pfam; PF02034; TWIK_channel; 1.
Pfints; PR01333; 2POREKCHANEL.
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MEDLINE=99069613; PubMed=9851916;
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236 GAFLNLVVLRFMTMNAED 253
| :||:|| || ||::
243 SACVNLLVLGFMASNADE 260
                                                                                           176 AAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVI 235
                                                                         183 YMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIMFILIGLAVF 242
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                                                                                                                                                                   124 MFQSLGERINTLVRYLLHRAKKGLGMR----RADVSMANMVL----IGFFSCISTLCIGA 175
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Search completed: August 28, 2001, 17:12:47 Job time: 416 sec

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CIW3_RAT
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CIW1_HUMAN
TWK8_CAEEL
TOK1_YEAST
YWS1_CAEEL
TOK1_YEAST
YWS1_CAEEL
TOK1_HUMAN
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CIQ1_HUMAN
CIQ1_HIME
YIFK_SALTY
QOX1_BACSU
SXR5_MOUSE
P1T_RHIME
Y71B_METJA
YSY3_RHIME
COBD_SYNY3
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01-OCT-2000 01-OCT-2000 POTASSIUM CO	01-OCT-2000 (Rel. 01-OCT-2000 (Rel. POTASSIUM CHANNEL CHANNEL PROTEIN TH	40, Last 40, Last 5UBFAMIL REK-1) (TI	ALL ALL SET	01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTW: CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM C:	٠	RECTIFYING POTASSIUM NNEL TPKC1) (TREK-1 K+		
CHANNEL SUBUNI KCNK2 OR TREK.	SUBUNIT). ? TREK.							

DOMAIN 144 170 PORE-FORMING (BY WILARLTY).	FT DOM	
	FT TRA	
۳.		
Ionic channel; Transmembrane; Ion transport; [tassium transport;]	KW Ion	
PRINTS; PR01333; 2POREKCHANEL.		
InterPro: IPR003280;		
InterPro; IPR001622;	DR Int	
603219;	_	
AF004711; AAD01203.1;		
EMBL; AF129399; AAD47569.1;	DR EMB	
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e by non-profit institutions as long a. : ; content is in no way	CC use	
ween the Swiss Institute of Bioinformat	CC bet	
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CHANNELS	දි :-	
	-i-	
CHLOROFORM, HALOTHANE AND ISOFLURANE.		
- MISCHELLGEAR LOCATION: INTEGRAL MEMBRANE STORM (POTENTIAL).	36	
SUBUNIT: HOMODIMER (POTENTIAL).		
to the EMBL/GenBank/		
Price L.A. Hellings S.E. Havashi J.H. Pal. 1. M.H.:	RA Pri	
REQUENCE FROM N.A.		
Nat. Neurosci. 2:422-426(1999).		
"Inhalational anesthetics activate two-pore-dom.in background K+	RT "In	
SEQUENCE FROM N.A.		
NCBI TAXTD=4606.	OX NOT	
Chordata; Craniata; Vert.:a;		
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CIW2_MOUSE
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Best Local Similarity
Matches 405; Conser
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                                                                                                      01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTWARD RECTIFYING CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL TPKC1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
TRANSMEM
                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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DOMAIN
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TRANSMEM
                    TISSUE=Brain;
MEDLINE=97157476;
                                                                                                 CHANNEL
                                                                                                                                                     CIW2_MOUSE P97438;
            Fink
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 Lazdunski
                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                          376
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                                                                                                 SUBUNIT).
           Duprat F.,
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426
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193
224
253
288
309
378
                                                                              (Mouse)
                                                                                                                                                             STANDARD;
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                   PubMed=9003761;
                                                              Chordata;
Rodentia;
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134
16
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391
411
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           Lesage
                                     FUNCTION,
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N-LINKED (GLCNAC...) (
MISSING (IN REF. 2)...
RLV -> DWL (IN REF. 2).
S -> N (IN REF. 2).
A -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2062; D
Pred. No. 1.1e
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PORE-FORMING
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                     AND
                                                                                                                                                             PRT;
                                                             Craniata; Vertebrata;
Sciurognathi; Muridae;
           Reyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2ABA2336D4009F4E CRC64;
                                     TISSUE
          R.,
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nes 3;
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           Romey
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           Heurteaux
                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                              Murinae;
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                                                                                                         FOTASSIUM
TREK-1 K+
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Query Match
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Matches 395
                                                                                                          CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                   TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, functional expression and brain levilization unconventional outward rectifier K+ channel. EMBO J. 15:6854-6862(1996).
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                               Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U73488; AAC53005.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   channels."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patel A.J., Honore E., Les
"Inhalational anesthetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fink M., Duprat
Lazdunski M.;
                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lazdunski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
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                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION
                                                                                                                                                                                                                                                                                                           [onic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: INVEGRAL MEMBRANE TEIN (POTENTIAL TISSUE SPECIFICITY: HIGH EXPRESSION IN BUT AND LUNG. ALSO DETECTED IN KIDNEY, HEART AND SKELETAL MITTE. NOT DETECTED LIVER. IN THE BRAIN, HIGHEST EXPRESSION TO LEACTORY BULB, HIPPOCAMPUS AND CEREBELLUM.

MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE OF ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOFLURANE.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: OUTWARD RECTIFYING POTASSIUM CH. MEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANNELS
                                                                                                                                                                                                                                                                                                                                                                  MGI:109366; Kcnk
Neurosci.
                                                395;
                                                                                                                                                                                                                                                                                                                                  PF02034; TWIK_channel;
                                                            Similarity
                                                                                                                                                                                                                                                                                                                        PR01333;
                                                                                                                                                                                                                                                                                                                                              IPR003280;
                                                                                                      95
119
411
                                                                                                                                                                                                                                                                                                                                                          IPR000099; -. IPR001622; -.
                                                Conservative
                                                                                                           AA;
                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2:422-426(1999).
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                                                                                                                                                                                                                                                                                                                        2POREKCHANEL.
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67
155
177
207
208
268
293
411
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                                                                                                             45297
                                                            97.2%;
96.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTEGRAL MEMBRANE "TEIN (POTENTIAL).
IGH EXPRESSION IN BRAIN AND LUNG. ALSO
BART AND SKELETAL MY TE. NOT DETECTED
HIGHEST EXPRESSION "LFACTORY BULB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activate
                                                                                                             ¥.
                                               12;
                                                                                                                                                        POTENTIAL.

CYTOPLASMIC (PC., TIAL).

POTENTIAL.

PORE-FORMING (PC. TIAL).

POTENTIAL.

CYTOPLASMIC (PC. TIAL).

ESSENTIAL FOR C: TROFORM A

SENSITIVITY.
                                                            Score
Pred.
                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; 8F976DDD103EFA05 CRC64;
                                                                                                                                                 REQUIRED FOR BASAL CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                  CYTOPLASMIC ( PL
                                                                                                                                                                                                                                                          PORE-FORMING (1
                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                           Ion transport; Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reyes
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fink
                                                            2041;
No. 2
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-pore- ፫ ኒክ background
                                                           DB(1)
2.7e-129;
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                                                                                                                                                                         AND
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                                                                                                                                                                                                                                                                                                            transport;
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                                                                                                                                                                         HALOTHANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                               Gaps
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                          EMBL;
                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S. "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 11."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Frontal cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11042359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assignment of KCNK4 encoding the human potassium channel TRAAK to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361
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                                                                                                                                                                                                                                                                                                                 FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARD POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
SUBGUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INVEGRAL MEMBRANE PROTEIN (POTE SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF
                                                                                                                                                                                                                                                                                                   CHANNELS
                                       : AF248242;
: AF247042;
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                     18242; AAG31731.1;
17042; AAF64062.1;
IPR001622; -.
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Best Local
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TRANSMEM
                                              MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F., I "Inhalational anesthetics activate
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                                                                                                                                                                                                                                                                           MEDLINE=98292450; Prink M., Lesage F.,
                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
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Eukaryota; Metazoa;
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SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE.
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                                          LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
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channel; Transmembrane; Ion transport; Potassium transport;
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IPR003280; -
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LONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
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MISSING (IN ISOFORM 2);
478AB34B7B7AEC92 CRC64;
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Pred. No. 5.1
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Query Match Best Local s Matches 106

Similarity

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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACII 10)
CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID- 10)
KCNK5 OR TASK2.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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J. Biol. Chem. 273:30863-30869(1998).
                                                                                                                                                                                                                                               Glycoprotein.
                                                                                                                                                                                                                                                                                            Pfam; PF02034; TWIK_channel; 1 PRINTS; PR01333; 2POREKCHANEL
                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. See by and for commercial entities requires a license agreement (See by 5 //www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=99030343;
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Mammalia; Eutheria; Primates; Catarrhini; H
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SIMILARITY: BE
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL KCNO1)
KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                     Desir G.V., Orias M.,
Submitted (APR-1997)
                                                                                                                                                                                               Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.; "Sequence and function of the two P domain potassium implications of an emerging superfamily."; J. Mol. Med. 76:13-20(1998).
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                       MEDLINE=98122696; PubMed=9462864;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                     EMBO J.
                                                                                                                                                                                                                                                                                              "TWIK-1, a ubiquitous novel structure.";
                                                                                                                                                                                                                                                                                                                      Barhanin J.
                                                                                                                                                                                                                                                                                                                                         MEDLINE=96183184;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                     TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                 Lesage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                             MILTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

SUBLIBERAL ACIDIFICATION. WARDLED BY BARIUM, OF POTASSIUM CHANNEL.

SUBJUNIT. HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.

MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
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                                                                                                                                                                                                                                                                                                                                Guillemare
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008581;
01-0CT-2000
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01-OCT-2000 (Rel. 40, Cre 01-OCT-2000 (Rel. 40, Las 01-OCT-2000 (Rel. 40, Las POTASSIUM CHANNEL SUBFAMI CHANNEL PROTEIN TWIK-1).
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TISSUE-Brain;
                              SEQUENCE FROM N.A
                                                                                  NCBI_TaxID=10090;
                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003280;
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IPR001779;
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40, Last annotation updat
SUBFAMILY K MEMBER 1 (IN-
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                                                                                                                    Chordata;
Rodentia;
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32.5%;
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CYTOPLASMIC (
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PORE-FORMING
POTENTIAL.
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Pred. No. 1.
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T->A: NO EFFECT, JN CHANNEL
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PORE-FORMING
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                                                                                                              Craniata; Vertocrata;
Sciurognathi; Noridae;
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                    Murinae;
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                                                                                                                                                                                                  SEQUENCE
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-!- FUNCTION: WEAK INWARDLY RECTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98218573; PubMed=9559671;
Arrighi I., Lesage F., Scimeca J.-C.
"Structure, Chromosome localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-129/SVJ; T
MEDLINE-98218573;
                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The The Theorem 19 and 19 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse twik K+ channel gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS
                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:109322; Kcnk1.
InterPro; IPR000099; -.
InterPro; IPR001622; -.
InterPro; IPR001779; -.
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lesage F., Lauritzen
Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97165959; PubMed=9013852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The structure,
                                                                                                                                                                                                                                                                  RANSMEM
  25
                                             51
                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION IN BRAIN,

KINNEY, THYROID, SALIVARY GLAND, ADREMAL GLAND, PROSTATE,

EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE

EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND

OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL

MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN

CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS CONCEPTION. EXPRESSION INCREASES FROM 2-8 DA STABILIZES AFTER DAY 8.
MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C SIMILARITY: BELONGS TO THE TWO PORE DOMAIN F
                             FLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced sen the Swiss Institute of Bioinformatics and
FLVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF033017; AAC16973.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F02034; TWIK_channel; 1.
PR01096; TWIK1CHANNEL.
PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003280; -
                                                                                                                                                                                             1
21
104
133
154
178
212
247
268
95
336 ;
                                                                                    Conservative
                                                                                                                                                                                                  AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function and distribution of the mouse TWIK-1 K+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBITED BY QUININE, BARIUM, AND I ACTIVATED BY PROTEIN KINASE C. LONGS TO THE TWO PORE DOMAIN FAMILY
                                                                                                                                                                                                                         20
41
130
153
177
198
238
238
336
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                                                                                                      17.6%;
33.9%;
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                                                                                                                                                                                                  ₹,
                                                                                  Score 370.5;
Pred. No. 4.9e
57; Mismatches
                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                      PORE-FORMING (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                      PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ion transport; Potassium
                                                                                                                                                                                               A996060A18266FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reyes R., Fink M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carle G.F. and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ng as its content is in
                                                                                    ..9e-18;
ies 94;
                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                    (POTENTIAL).
                                                                                                                             DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G.F., Barhanin J.
ssue distribution
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DAYS AFTER
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                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through
                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S POST
                                                                                    Gaps
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RESULT 8
CIW3_HUMAN
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACIT: 'NSITIVE POTASSIUM
CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENS, IVE K+ CHANNEL).
                                                                    MIM; 603220; -.
                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      014649;
                                                                                                                                      or send an
                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99254548; PubMed=10321245;
Patel A.J., Honore E., Lesage F., Fink M., Rom: G., Lazdunsk:
"Inhalational anesthetics activate two-pore-domain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duprat F., Lesage F., Fink M., Reyes R., Heurtenux C., Lazdunski M.; "TASK, a human background K+ channel to sense external pH variations near physiological pH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CIW3_HUMAN
                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97459932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCNK3 OR TASK.
                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissue=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGN
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185 FAAVL 289
186 MLVVL 264
188 MLVVL 264
189 MAN STANDARD; PRT; 394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          ROUNTION: PH-DEPENDENT, VOLTAGE-INSENSITIV, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION FOR STANE ACTS AS AN ION CONCENTRATION ON EITHER SIDE OF THE MORENTATION IS LOW. WHEN EXTERNAL POTASSIUM ONCENTRATION IS INWARD CONCENTRATION IS INWARD. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE OF THE MORENTIAL).

TISSUE SPECIFICITY: WIDESPREAD EXPRESSION TO STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. LOW. EXPRESSION IN BRAIN, LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SOME THE MORE OF THE MALE OF THE MORE OF THE MALE OF THE MORE OF THE M
                                                                                                                                                                                                                                                                                                                                           CHANNELS
                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TWO PORE DOMA-
                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: INHIBITED BY EXTERNAL ACTUAL HALOTHANE AND ISOFLURANE.
                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is pr. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               physiological pH.";
J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNYGVSVLSNASGN-WNWDETSALFEASTVLSTTGY( 34, L)DGGKAFCIIYSVIGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GS
                                                                                                       non-profit institutions as long of sconcern non-profit institutions as long of the by and for commercial and this statement is not removed. We will by and for commercial and this statement (See the will wow isb-sib.ch/announce/
                                                                                                                                                                                                                                                                  the Swiss Institute
                                             IPR000099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9312005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vert brata; Euteleostomi;
                                                                                                                                                                                                                                                          of Bioinformatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ik пiнidae;
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                                                                                                                                                                                                                                                                            Shed through a collaboration
                                                                                                                                                                                                                                                                                                                                                                  AMILY OF POTASSIUM
                                                                                                                                                                                                                                                                  and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lazdunski
                                                                                                                                                                                                                                                                  EMBL
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Best Local :
                                                                                                                                                                                                   Q9Y257;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 6 (INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-2) (TWIK-ORIGINATED SIMILARITY SEQUENCE).
KCNK6 OR TWIK2 OR TOSS.
                                                           MEDLINE-99285568; PubMed-10359073; Pountney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes Saganich M., Rudy B., Artman M., Coetzee W.A.; "Identification and cloning of TWIK-originated similarity (TOSS): a novel human 2-pore K+ channel principal subunit. FEBS Lett. 450:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
 Chavez
Mehta 1
                                                                                                                                                                                                                                                                                                  HUMAN
                    MEDLINE=99175162; PubMed=10075682;
                                           SEQUENCE FROM
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel;
                                                                                                                                 TISSUE=Testis;
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                                                                                                      157
                                                                                                                                                                                                                                                                                                                                                                                                                                 109
                                                                                                                                                                                                                                                                                     [W6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                          QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTRN
                                                                                                                                                                                                                                                                                                                                                             LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T
                                                                                                                                                                                                                                                                                                                                                                                   ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
                                                                                                                                                                                                                                                                                                                                                                                                FCIIYALLGIPLFGFLLAGVGDQLGTIF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELERVYLRL-KPHKAGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI
                                                                                                                                                                                                                                                                                                                                                                                                                               FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD---
 z R.A., Gray A.T.,
Y., Forsayeth J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
108
129
159
184
223
244
53
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                                                                                                                                                                                             (Human)
                                          N.A.,
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                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
29
101
128
158
179
207
243
394
43518
                                                                                                                                                                         Chordata;
Primates;
                                          AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.3%;
Zhao B.B.
                                          MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 363;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P
9FF4C8266F615FB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ion
                                                                                                                                                                       Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PORE-FORMING
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                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
· s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport;
         Kindler C.H.,
                                          OF.
                                                                                                                                                                                                                                                                                     313
                                          CYS-
                                                                                                                                                                                     Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.8e-17;
                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GKGIAKVEDTFIKWNVSQTKIRI
                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
          Mazurek M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                         Holmes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport;
                                                                                   sequence
                                                                                                         U
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                                                                                                                                                                                                                                                                                                                                                                                                                               MSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         266
                                                                                                                                                                                                                                                                                                                                                                                                                               156
                                                                                                                                                                                                                                                                                                                                                                                                                                                     208
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Best Local
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EMBL; AF117708;
MIM; 603939; -.
                                                                                                                                                                                                                                                                              MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potassium channel family.";
J. Biol. Chem. 274:7887-7892(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mehta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chavez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM
                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                              fonic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "TWIK-2, a new weak inward rectifying.
                                                                                                                                                117
           289
                               193
                                                                             137
                                                                                                    173
                                                                                                                          77
                                                                                                                                                                        17
                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinform
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SÜBCELLULÄR LOCATION: INTEGRAL MEMBRANE FROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
TESTED EXCEPT FOR SKELETAL MUSCLE. STROKEST EXPRESSION IN
PLACENTA, PANCREAS, HEART, COLON AND SP. 1.33, LOWER LEVELS DETECTED
IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, I CER, KIDNEY AND THYMUS.
LOWEST EXPRESSION DETECTED IN BRAIL.
MISCELLANEOUS: INHIBITED BY INTERNAL ACTIVITICATION AND, TO A SMALL
DEGREE, BY ZINC. NOT INHIBITED BY QUINIE, QUINIDONE OR BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: WEAK INWARDLY RECTIFYING POTAS; TUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                              YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIP
                               AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPY -
                                          LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTITTLFGCVLFVA--LPAIIF
                                                                                                                                               LGNTSNQIS----HWDLGSSFFFAGTVITTIGFGNISPKTEGGKIFCIIYALLGIPLFGF
                                                                                                                                                                        YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCV^APALDAFVERVLAAGRLGRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Υ.,
                                                                             LLTASAQRLSLL - - -
                                                                                                                          LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPL: DAGKAFSIAFALLGVPTTML
                                                                                                                                                                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.A.,
                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            PR01096; TWIK1CHANNEL. nannel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1., Gray A.T., Zhao B.B., Ki
Forsayeth J.R., Yost C.S.;
Shem. 274:24440-24440(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001622;
                                                                                                                                                                                                                                                                              90
121
142
173
199
236
257
79
85
85
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD22980.1;
AAD24000.1;
                                                                                                                                                                                                                                                                           25
115
141
141
172
193
223
223
223
256
313
79
85
85
83
                                                                                                                                                                                                                               16.6%;
                                                                             -LTHVPLSWLSMRWGWDPRRAACW + WALLGVVVTVCFLVPAVIF
                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (1
POTENTIAL.
PORE-FORMING
                                                                                                                                                                                                                                Score 348;
Pred. No. 1
                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
C->A: NO CHANNUE. ACTYVTY.
1379382DFB057 DF CRC64;
                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ion transport;
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kindler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See h.
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                                                                                                                                                                                                                                . 4 e
                                                                                                                                                                                                                                                                                                                           (POTERTIAL)
                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                           , J. HG
                                                                                                                                                                                                                                                                                                                                                  (POTIENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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KPVVMEWILVGLAYFAAV 2
                                                                                                                                                                                                                     104
                                                                                                                                                                                                                                 .6;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usaye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i:://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ١٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                         Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mazurek M.J.,
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                    Gaps
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RESULT
CIW3_MC
CIW3_MOUSE STANDARD; PRT; 409 AA.

035111; 035163;

01-OCT-2000 (Rel. 40, Created)

01-OCT-2000 (Rel. 40, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

POTASSIUM CHANNEL SUBFAMILY K MEDIASE 3 (ACID-SENSITIVE |

CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ C|

(CARDIAC TWO-PORE BACKGROUND K+ CHANNEL) (CTBAK-1).

KCNK3 OR TASK OR CTBAK
                                                                                                    EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license additional entities and the second entities of the second entities and the second entities and the second entitle entities and the second entities and the second entitle entitle entities and the second entitle e
                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Proton block and voltage gating are cardiac leak channel kcnk3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Heart;
MEDLINE-98165556; PubMed-9506712;
Kim D., Pujita A., Horio Y., Kurachi Y.;
"Cloning and functional expression of a novel cardiac background K+ channel (cTBAK-1).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO
     InterPro;
                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duprat F., Lesage F., Fink M.,
"TASK, a human background K+ c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20287574; PubMed=10748056; Lopes C.M., Gallagher P.G., Buck M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-409 FROM N.A. MEDLINE=97459932; PubMed=93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DI
IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALI
INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLI
MISCELLANEOUS: INACTIVATED BY BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liac leak chainel Author (275:16978) (2000).

SIOLI Chem. 275:16978 (2000).

SIOLI Chem. 275:16978 (2000).

FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
                                                                                                  AB008537; BAA25436.1;
AF006824; AAC53367.1;
AB013345; BAA28349.1;
AF241798; AAF81418.1;
AF242508; AAF81418.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                   European
                                                                                  MGI:1100509;
                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EW
European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            physiological pH.";
J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              round K+ channel (cTBA
Res. 82:513-518(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a human background K+
hysiological pH.";
                                                                                                                                                                                                                                                                                                                non-profit
and this st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa; Chordata;
Eutheria; Rodentia;
                                                       IPR000099;
                                                                            Kcnk3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9312005;
F., Fink M., Reyes
ckground K+ channel
                                                                                                                                                                                                                                                                                                                                        institutions as long
                                                                                                          JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                potassium-dependent
                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Butler M.H.,
                                                                                                                                                                                                                                                                                                                                   There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sense external
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                                                                                                                                                                                                                                                                                                              Usage
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ndent in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHANNEL)
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pH variations
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                                                                                                                                                                                                                                                                                                                                                                                           EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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RESULT 1
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Best Local
                                                                                                                                                                                                                                            CIW3_RAT
054912;
                            Leonoudakis D., Gray A.T., Winegar B.D., K
Taylor D.M., Chavez R.A., Forsayeth J.R.,
"An open rectifier potassium channel with
cloned from rat cerebellum.";
J. Neurosci. 18:868-877(1998).
                                                                                                                                                                                      01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K + C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
                                                                                        TISSUE=Cerebellum;
MEDLINE=98099797;
                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                               KCNK3 OR TASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01095; TASKCHANNEL. PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                           217
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         CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM ION CONCENTRATION ON EITHER SIDE OF THE HER-BRANE. ACTS
                                                                                                                                                                                                                                                                                                         QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTHN
                                                                                                                                                                                                                                                                                                                                                ELERVVLRL-KPHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERORI LRQLELRARYNLSEGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKWKTVSTIFLVV--VLYLLIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T
                                                                                                                                                                                                                                                                                                                            LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKF LYGEFRAHAAEWTAN 320
                                                                                                                                                                                                                                                                                                                                                                                  FCMFYALLGIPLTLVMFQSLGERI------NTF ( ) LLHRAKRGLGMRHAEVSM
                                                                                                                                                                                                                                                                                                                                                                                                                FCIIYALLGIPLEGELLAGVGDQLGTIFGKGIAKVEDTFI; WNVSQTK-----IRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAG: VITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF02034; TWIK_channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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78
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244
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                                                                                            PubMed=9437008;
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101
128
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                                                                       Winegar B.D., Kindler Forsayeth J.R., Yost C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                            VOLTAGE-INSENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
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CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
                                                                                                                                               Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PORE-FORMING
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-> I (IN REF.
35236E011AACF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport; F assium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343; DB 1
No. 4.1e-1
POTASSIUM
                                                                                                                                                                                                                                                       411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Pr TELLIAL)
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16;
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                                                             pore
 CONCENTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 409;
                                                                       C.H.,
                              BACKGROUND
                                                             domains
                                                                                                                                                                                         K+ CHANNEL).
                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                               Murinae;
                                                                                  Harada
                                                                                                                                                                                                   POTASSIUM
         S AS AN
                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                              POTASSIUM
                                                             tandem
                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                            156
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RESULT 12
ORK1_DROME
ID ORK1_D
AC Q94526
DT 01-OCT
DT 01-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 88
     ORK1_DROME
Q94526;
Q1-OCT-2000
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PFUZUU...
PRINTS; PRO11905; TASNU....
PRINTS; PRO1333; 2POREKCHANEL.
PRINTS; PRO1333; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF031384; AAC39952.1; -. InterPro; IPR000099; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003092;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001622;
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                                                                                                                                                                                                                157
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(BY SIMILARITY).

SUBCELLULAR LOCATION: INTEGR
TISSUE SPECIFICITY: STRONGES
EXPRESSION IN LUNG AND BRAIN
SKELETAL MUSCLE.

MISCELLANEOUS: INHIBITED BY
BUPITACAINE AND PHENYTOIN. A
SMILARITY: BELONGS TO THE T
CHANNELS.
                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                          MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T 97
                                                                                                                                             QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTHN
                                                                                                                                                                          LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTAN
                                                                                                                                                                                                                                  MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLELRARYNLSEGGYE
                                                                                                                                                                                                                ANMVLIGFVSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
                                                                                                                                                                                                                                                                                  FCMFYALLGIPLTLVMFQSLGERI---
                                                                                                                                                                                                                                                                                                                   FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTK-----IRI
                                                                                                                                                                                                                                                                                                                                                     ELERVVLRL-KPHKAGV--
                                                                                                                                                                                                                                                                                                                                                                                      ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity
88; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003280;
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     (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                         STANDARD;
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Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTEGRAL MEMBRANE PROTEIN (POTENTIAL). TRONGEST EXPRESSION IN HEART. MODERATE ID BRAIN. LOW LEVELS IN LIVER, KIDNEY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 343; DB 1;
Pred. No. 4.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY EXTRACELLULAR ACIDIFICATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ion
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LINKED (GLCNAC...) (P
D2778016E09E2BF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATED BY PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                 -----NTFVRYLLHRAKRGLGMRHAEVSM
                                                                                                                                                                                                                                                                                                                                                    -QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transport; Potassium
                                                         1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                             267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
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RA Addams M.D., Celniker S.E., Holt R.A., Evans ... Gocayne J.D., Addams M.D., Celniker S.E., Holt R.A., Evans ... Gocayne J.D., RA Addams M.D., Celniker S.E., Holt R.A., Wilson J.A., A., Galle R.F., RA George R.A., Lewis S.E., Flottard S., Asbburre, M., Henderson S.N., RA Brandon R.C., Rogers Y.-B.C., Blazej R.G., C.-W.M., Pfelifer B.D., RA Ballew R.M., Basu A., Baxendale J., Bayrak. Flow, Miklos G.L.G., RA Abril J.F., Apbayani A., An H.-J., Andrews-Prakoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayrak. Flow, Chent. C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayrak. Flow, Chenter A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Detter A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Detter A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Detter A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Devices P., RA Bockson K.Y., Benos P.Y., Berman B.P., Bhandur P., Detter A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Davies P., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Davies P., Cherry J.M., Cawley S., Dahlke C., Davanpor ... Davies P., Chent A., Chandra I., Chent R.A., Chent R.A., Deng Z., Mays A.D., J. L. Dietz S.M., Bodson K.A., Dong E., Gorrell J.H., Gu Z., Guz ... Chent R.A., Chent R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; 14;5°, oda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera: ...chycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97075152; PubMed-8917578; Goldstein S.A.N., Price L.A., Rosenthal D.H. Ostassium-selective leak channel v. cloned from Drosophila melanogaster by expressioned
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Adams M.D., Celniker S.E., Holt R.A.,
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                                                                              IS REVERSED.
SUBCELLULAR LOCATION: INTEGRAL
TISSUE SPECIFICITY: WIDESPREAD
EXPRESSION IN MUSCLE, BRAIN AND
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RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (7.5)
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      AMILY
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AT LOW LEV
      POTASSIUM
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Best Local :
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       Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                              Q9ZZTI; Q9R242; Q9R1VI; Q9QYE8; Q9QXYO;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 8 (POTATIVE POTASSIUM CHANNEL DP3) (DOUBLE-PORE K+ CHANNEL 3) (NEUROMUSCULAR TWO P DOMAIN POTASS:
                                                                                                                                                   _MOUSE
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CARBOHYD
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                                                                                                                                                                                              VGYLRRMLN-ELY
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                                         OR KCNK6 OR DPKCH3 OR KNOT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pean Bioinformatics Institute. There are no restrictions non-profit institutions as long as its content is in and this statement is not removed. Usage by and for cor
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Sciurognathi;
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EMBL; AF110521; AAD29577.1;
EMBL; AB015729; BAA35074.1;
EMBL; AF022820; AAD09337.1;
EMBL; AF012324; AAF21603.1;
EMBL; AF158234; AAF14528.1;
                                Glycoprotein.
DOMAIN
                                                                                                   MGD;
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is proved through between the Swiss Institute of Bioinformatic: and the EN the European Bioinformatics Institute. There we no restrain
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"Cloning of a new double-pore
tesis.";
 TRANSMEM
                                                                                                                                                                                or send an
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           DOMAIN
                       TRANSMEM
                                                                   PRINTS;
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[1]
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TISSUE SPECIFICITY: DETECTED IN EMBRYO, TYL LUNG AND LIVER.
WEAKLY EXPRESSED IN COLON, TESTIS, ATRIA. NUMBEY, INTESTINE,
BLADDER, UTERUS, OVARY, SALIVARY GLAND, HAVING AND BRAIN STEM.
DETECTED IN BRAIN, CEREBELLUM, SPINAL COVA. 4EART, VENTRICLE,
SKELETAL MUSCLE, LIVER, PLACEMTA AND DANGELS. IN THE EXE, HIGH
EXPRESSED IN THE RETINAL GANGLION CELL LAYER AND INNER NUCLEAR
                                                                                                                                                                                                                                                                        SIMILARITY: CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PROBABLE POTASSIUM CHANNEL SUBJUDE NO CHANNEL ACTIVITY OBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICULUM MAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER TO REACH THE PLASMA MEMBRANE.
                                                                                                     MGI:1341841;
                                                                   PR01333;
                                                                                                                                                                                                    non-profit institutions as long and this statement is not removed
                                                                IPRO03280; -.
R01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               localization, channel KCNK6
                                                                                       IPR001622; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                               email to license@isb-sib.ch)
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274:11751-11760(1999).
                                                         Transmembrane;
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R., Lesage F., F
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118
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                                                                                                                                                                                         license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      potassium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang L.-Y.
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                                                       transport; !-
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                                                        transport;
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Best Local Similarity
Matches 82; Conser
      homologue with a unique pore structure.";

J. Biol. Chem. 274:11751-11760(199).

-!- FUNCTION: PROBABLE POTASSIUM CHANNEL SUFTIONS OBSERVED IN VITRO AS PROTEIN REMAINS IN MAY NEED TO ASSOCIATE WITH AN AS YET UNK REACH THE PLASMA MEMBRANE.

-!- SUBUNIT: HOMODIMER (POTENTIAL).

-!- SUBUNIT: HOMODIMER (POTENTIAL).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE

-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHC PRODUCED BY ALTERNATIVE SPLICING.

-!- SIMILARITY: BELONGS TO THE TWO PORE DOMA CHANNELS.
                                                                                                                                                                                                                                                                                                                  V7_HUMAN S'
CIW7_HUMAN S'
Q9Y2U2; Q9Y2U4; O1-OCT-2000 (Rel
01-OCT-2000 (Rel
01-OCT-2000 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CONFLICT
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TRANSMEM
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                                                                                                                                                                                  Salinas M.,
                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                       POTASSIUM CHANNEL SUBFAMILY K MEMBER
                                                                                                                                                       "Cloning of a new mouse two-P domain channel subunit
                                                                                                                                                                      Lazdunski M.;
                                                                                                                                                                                            MEDLINE-99223496;
                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               233
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                                                                                                                                                                                                                                                                                                                                                                                                                               LGQFALLGYLLLGL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGAVLRAQAHGVSSLGNGS-ETSNWDLPSALLFTASILTTTGYGHMAPLSSGGKAFCVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WARYLLLLMAHLLAMGLGAVVLQALEGPPARHLQAQVQAELASFQAEHRACLPPEALEEL
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173
199
233
254
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(Rel. 40, Last sequence up)
(Rel. 40, Last annotation)
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                     HOMODIMER (POTENTIAL).

LAR LOCATION: INTEGRAL MEMBRANE PROTEIN
IVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE)
BY ALTERNATIVE SPLICING.
BY ALTERNATIVE SPLICING.
TY: BELONGS TO THE TWO PORE DOMAIN FAMIL
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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193
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232
293
32168
                                                                                                                                                                                                                                                                                                                                                      Q9Y2U3;
                                                                                                                                                                                            PubMed=10206991;
                                                                                                                                                                                                                                                       Chordata; Primates;
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28.98;
                                                                                                                                                                               Lesage F., Fosset M., Heurteaux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
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POTENTIAL.

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-STR (IN REF. 4).

GS -> TR (IN REF. 4).

GS -> THSREEGERGOEFGTR (IN RIGG).

GS -> STHSREEGERGOEFGTR (IN RIGG).

GS -> STHOREFE. 2 3, 4 AND 19 COTENTIAL.

T -> P (IN REF. 2).

T -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 296.5; DB 1;
Pred. No. 3.8e-13;
7; Mismatches 94;
                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   567D32AE355BA44F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              -LAVETFSELPQVRA
                      PORE DOMAIN FAMILY
                                                                                                                                                                                                                                                                                                               on update)
                                                                                                                                                                                                                                                                                                                                                                  307
                                                                                            SUBUNIT. NO CHANNEL ACTIVITY IN THE ENDOPLASMIC RETICULUM UNKNOWN PARTNER IN ORDER TO
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                                            HERE),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                        (POTENTIAL)
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D 5).
                                            AND C;
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                     POTASSIUM
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                                             ARE
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Best Local
Matches 8
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                                                                                                                               _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
SEQUENCE
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DOMAIN
TRANSMEM
        Rhabditidae; Peloderinae; NCBI_TaxID=6239; [1]
                                                          TWK-8 PROTEIN.
TWK-8 OR F22B7.7
                                                                            01-FEB-1994
15-JUL-1998
                                                                                                 P34410;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF110524; EMBL; AF110523;
                                     Eukaryota; Metazoa; Nematoda; Chromadorea;
                                               Caenorhabditis elegans
                                                                                                                    TWK8_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 603940;
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                                                                                                                                                                                        277
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                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                        Match
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                                                                                                                                                                               ----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEF
                                                                                                                                                                                                                                                                    ALLGIPLEGELLAGVGDQLGTIEGKGIAKVEDTFIKWNV> "KIRIISTIIFILEGCVLF 222
                                                                                                                                                                                                                                                                                                  WSRYGLLVVAHLLALGLGAVVFQALEGPPACRLQAELRALLAAFQAEHRACLPPGALEEL
                                                                                                                                                                                                                                                 AALGLPASLALVATLRHCLLPVLSRPRAWVA---VHWQI
                                                                                                                                                                                                                                                                                        LGTALATQAHGVSTLGNSSEGRT-WDLPSALLFAASILTTTGYGHMAPLSPGGKAFCMVY
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                258
307
                                                                                     (Rel.
                                                                                                                                                                                                                                                                                                                                                                     Conservative
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; AAD29580.1;
; AAD29579.1;
                                                                                                                    STANDARD;
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31946
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257
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                                                                                                 Created)
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                             Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                    Score 291.5; DB 1
Pred. No. 8.2e-13:
3; Mismatches 111
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CYTOPLASMIC
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING
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YLLLGLLAMLLA -> GGTSLQGTAWEG (IN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (
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MISSING (IN ISC+ DRM
BD4A36DD9591ADAC C
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                                                                                                                    PRT;
                                                                             on update)
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                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
111;
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                                      , ',ditida;
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                                       Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                  182
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                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 10.4%; Score 217.5; DB 1; Length 335; Best Local Similarity 26.7%; Pred. No. 7.7e-08; Matches 60; Conservative 37; Mismatches 75; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
Nature 368:32-38(1994).
"!- SIMILARITY: TO POTASSIUM CHANNEL PROTEIN HAK-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L12018; AAA65460.1; -.
                                                                                              131
187 MYIILLYIILGKFSMKKKQKFKIFLGLAITTMCIDLVGVQYIRKI 231
                                           265 EYLDF-----YKPVVWFWILVGLAYFAAVLSMIG-DWLRVI 299
                                                                                                                                     205 KIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDI 264
                                                                                                                                                                                                                          120 TSNQISH-----WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                        15 TSNEVKKNAATETWTFSSSIFFAVTVVTTIGYGNPVPVTNIGRIWCILFSLLGIPL---T 71
                                                                                         RI----PAFLVLAILIVYTAFGGVLMSKLEPWSFFTSFYWSFITMTTVGFGDLMPRRDGY 186
                                                                                                                                                                                   LVTIAD-LGKFLSEHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIEEK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F22B7.7; CE00160.
335 AA; 38472 MW; 27DE7F1E79B3CA29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shownkeen R.,
                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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